

Figure 1
The Genetic Code

First Position (5' end)	Second position				Third position (3' end)
	U	C	A	G	
U	Phe	Ser	Tyr	Cys	U
	Phe	Ser	Tyr	Cys	C
	Leu	Ser	Stop	Stop	A
	Leu	Ser	Stop	Trp	G
C	Leu	Pro	His	Arg	U
	Leu	Pro	His	Arg	C
	Leu	Pro	Gln	Arg	A
	Leu	Pro	Gln	Arg	G
A	Ile	Thr	Asn	Ser	U
	Ile	Thr	Asn	Ser	C
	Ile	Thr	Lys	Arg	A
	Met	Thr	Lys	Arg	G
G	Val	Ala	Asp	Gly	U
	Val	Ala	Asp	Gly	C
	Val	Ala	Glu	Gly	A
	Val	Ala	Glu	Gly	G

004280-9024960

Figure 2

GRVER51.SEQ A T G A T G A A A C G C G A A A A G A A C G T G A T C T A C G G C C C A G A A C 40
GR6.SEQ A T G A T G A A A C G C G A A A A G A A C G T G A T C T A C G G C C C A G A A C 40
GRVER5.SEQ A T G A T G A A A C G C G A A A A G A A C G T G A T C T A C G G C C C A G A A C 40
GRVER4.SEQ A T G A T G A A A C G C G A A A A G A A C G T G A T C T A C G G C C C A G A A C 40
GRVER3.SEQ A T G A T G A A A C G C G A A A A G A A C G T G A T C T A C G G C C C A G A A C 40
GRVER2.SEQ A T G A T G A A A C G C G A A A A G A A C G T C A T C T A C G G C C C A G A G C 40
GRVER1.SEQ A T G A T G A A A C G C G A A A A G A A C G T C A T C T A C G G C C C A G A G C 40
YG81-6G1.SEQ A T G A T G A A G C G A G A G A A A A T G T T A T A T A T G G A C C C G A A C 40
RDVER1.SEQ A T G A T G A A G C G T G A G A A A A A T G T G A T T T A T G G T C C T G A A C 40
RDVER2.SEQ A T G A T G A A G C G T G A G A A A A A T G T G A T T T A T G G T C C T G A A C 40
RDVER3.SEQ A T G A T G A A G C G T G A G A A A A A T G T C A T C T A T G G C C C T G A G C 40
RDVER4.SEQ A T G A T G A A G C G T G A G A A A A A T G T C A T C T A T G G C C C T G A G C 40
RDVER5.SEQ A T G A T G A A G C G T G A G A A A A A T G T C A T C T A T G G C C C T G A G C 40
RD7.SEQ A T G A T G A A G C G T G A G A A A A A T G T C A T C T A T G G C C C T G A G C 40
RDVER51.SEQ A T G A T G A A G C G T G A G A A A A A T G T C A T C T A T G G C C C T G A G C 40
RDVER52.SEQ A T G A T G A A G C G T G A G A A A A A T G T C A T C T A T G G C C C T G A G C 40
RD1561H9.SEQ A T G A T A A A G C G T G A G A A A A A T G T C A T C T A T G G C C C T G A G C 40

GRVER51.SEQ C A C T G C A T C C A C T G G A A G A C C T C A C C G C T G G T G A G A T G C T 80
GR6.SEQ C A C T G C A T C C A C T G G A A G A C C T C A C C G C T G G T G A G A T G C T 80
GRVER5.SEQ C A C T G C A T C C A C T G G A A G A C C T C A C C G C T G G T G A G A T G C T 80
GRVER4.SEQ C A C T G C A T C C A C T G G A A G A C C T C A C C G C T G G T G A G A T G C T 80
GRVER3.SEQ C A C T G C A T C C A C T G G A A G A C C T C A C C G C T G G T G A G A T G C T 80
GRVER2.SEQ C T C T G C A C C C A T T G G A A G A C C T G A C C G C T G G T G A G A T G T T 80
GRVER1.SEQ C T C T G C A C C C A T T G G A A G A C C T G A C C G C C G G T G A G A T G T T 80
YG81-6G1.SEQ C C C T A C A C C C C T T G G A A G A C T T A A C A G C T G G A G A A A T G C T 80
RDVER1.SEQ C A T T G C A T C C T C T G G A G G A T T T G A C T G C T G G C G A A A T G C T 80
RDVER2.SEQ C A T T G C A T C C T C T G G A G G A T T T G A C T G C C G G C G A A A T G C T 80
RDVER3.SEQ C T T T G C A C C C T T T G G A G G A T T T G A C T G C C G G C G A A A T G C T 80
RDVER4.SEQ C T T T G C A T C C T T T G G A G G A T T T G A C T G C C G G C G A A A T G C T 80
RDVER5.SEQ C T C T C C A T C C T T T G G A G G A T T T G A C T G C C G G C G A A A T G C T 80
RD7.SEQ C T C T C C A T C C T T T G G A G G A T T T G A C T G C C G G C G A A A T G C T 80
RDVER51.SEQ C T C T C C A T C C T T T G G A G G A T T T G A C T G C C G G C G A A A T G C T 80
RDVER52.SEQ C T C T C C A T C C T T T G G A G G A T T T G A C T G C C G G C G A A A T G C T 80
RD1561H9.SEQ C T C T C C A T C C T T T G G A G G A T T T G A C T G C C G G C G A A A T G C T 80

GRVER51.SEQ C T T C C G A G C A C T G C G T A A A C A T A G T C A C C T C C C T C A A G C A 120
GR6.SEQ C T T C C G A G C A C T G C G T A A A C A T A G T C A C C T C C C T C A A G C A 120
GRVER5.SEQ C T T C C G A G C A C T G C G T A A A C A T A G T C A C C T C C C T C A A G C A 120
GRVER4.SEQ C T T C C G T G C A C T G C G T A A A C A T A G T C A C C T C C C T C A A G C T 120
GRVER3.SEQ G T T C C G T G C C C T G C G T A A A C A T A G C C A C C T G C C T C A A G C T 120
GRVER2.SEQ G T T C C G T G C T C T G C G T A A A C A T T C T C A C T T G C C T C A A G C C 120
GRVER1.SEQ G T T C C G T G C T C T G C G T A A A C A T T C T C A C T T G C C T C A A G C C 120
YG81-6G1.SEQ C T T C C G T G C C C T T C G A A A A C A T T C T C A T T T A C C G C A G G C T 120
RDVER1.SEQ G T T T C G C G C C T T G C G C A A G C A C A G C C A T C T G C C A C A G G C T 120
RDVER2.SEQ G T T T C G C G C C T T G C G C A A G C A C A G C C A T C T G C C A C A A G C T 120
RDVER3.SEQ G T T T C G C G C T T T G C G T A A G C A C T C T C A T T T G C C T C A A G C C 120
RDVER4.SEQ G T T T C G T G C T T T G C G T A A A C A C T C T C A T T T G C C T C A A G C C 120
RDVER5.SEQ G T T T C G T G C T C T C G C A A G C A C T C T C A T T T G C C T C A A G C C 120
RD7.SEQ G T T T C G T G C T C T C G C A A G C A C T C T T A T T T G C C T C A A G C C 120
RDVER51.SEQ G T T T C G T G C T C T C G C A A G C A C T C T C A T T T G C C T C A A G C C 120
RDVER52.SEQ G T T T C G T G C T C T C G C A A G C A C T C T C A T T T G C C T C A A G C C 120
RD1561H9.SEQ G T T T C G T G C T C T C G C A A G C A C T C T C A T T T G C C T C A A G C C 120

Figure 2 (cont.)

GRVER51.SEQ C T C G T G G A C G T G G G A G A C G A G A G C C T C C T A C A A A G 160
 GR6.SEQ C T C G T G G A C G T G G G A G A C G A G A A C C T C C C T A C A A A G 160
 GRVER5.SEQ C T C G T G G A C G T G G G A G A C G A G A G C C T C C C T A C A A A G 160
 GRVER4.SEQ C T C G T G G A C G T G G G A G A C G A G A G C C T C T C T A C A A A G 160
 GRVER3.SEQ C T C G T G G A C G T G G G T G A C G A G A G C C T G T C T T A C A A A G 160
 GRVER2.SEQ C T G G T C G A T G T C G T G G G C G A C G A G A G C T T G T C T T A T A A G G 160
 GRVER1.SEQ C T G G T G G A T G T C G T G G G C G A C G A A A G C T T G T C T T A T A A G G 160
 YG81-6G1.SEQ T T A G T A G A T G T G G T T G G C G A C G A A T C G C T T T C C T A T A A A G 160
 RDVER1.SEQ T T G G T C G A C G T G G T C G G T G A T G A G T C T C T G A G C T A C A A A G 160
 RDVER2.SEQ T T G G T G G A C G T G G T C G G T G A T G A A T C T C T G A G C T A C A A A G 160
 RDVER3.SEQ T T G G T C G A T G T G G T C G G C G A T G A A T C T T T G A G C T A T A A G G 160
 RDVER4.SEQ T T G G T C G A T G T G G T C G G C G A T G A A T C T T T G A G C T A C A A G G 160
 RDVER5.SEQ T T G G T C G A T G T G G T C G G C G A T G A A T C T T T G A G C T A C A A G G 160
 RD7.SEQ T T G G T C G A T G T G G T C G G C G A T G A A T C T T T G A G C T A C A A G G 160
 RDVER51.SEQ T T G G T C G A T G T G G T C G G C G A T G A A T C T T T G A G C T A C A A G G 160
 RDVER52.SEQ T T G G T C G A T G T G G T C G G C G A T G A A T C T T T G A G C T A C A A G G 160
 RD1561H9.SEQ T T G G T C G A T G T G G T C G G C G A T G A A T C T T T G A G C T A C A A G G 160

GRVER51.SEQ A A T T T T T C G A A G C T A C T G T G C T G T T G G C C A A A G C C T C C A 200
 GR6.SEQ A A T T T T T C G A A G C T A C T G T G C T G T T G G C C A A A G C C T C C A 200
 GRVER5.SEQ A A T T T T T C G A A G C T A C T G T G C T G T T G G C C A A A G C C T C C A 200
 GRVER4.SEQ A A T T T T T C G A A G C T A C T G T G C T G T T G G C C A A A G C C T C C A 200
 GRVER3.SEQ A A T T T T T C G A A G C T A C T G T G C T G T T G G C C A A A G C C T G C A 200
 GRVER2.SEQ A A T T T T T C G A A G C T A C T G T C C T G T T G G C C A A A T C T C T G C A 200
 GRVER1.SEQ A G T T T T T C G A A G C T A C T G T C C T G T T G G C C A G T C T C T G C A 200
 YG81-6G1.SEQ A G T T T T T G A A G C G A C A G T C C T C C T A G C G C A A A G T C T C C A 200
 RDVER1.SEQ A A T T C T T T T G A G G C A A C C G T G T T G C T G G C T C A A A G C T T G C A 200
 RDVER2.SEQ A G T T C T T T T G A G G C A A C C G T G T T G C T G G C T C A G A G C T T G C A 200
 RDVER3.SEQ A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C T T T G C A 200
 RDVER4.SEQ A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C C T T G C A 200
 RDVER5.SEQ A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C C C T C C A 200
 RD7.SEQ A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C C C T C C A 200
 RDVER51.SEQ A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C C C T C C A 200
 RDVER52.SEQ A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C C C T C C A 200
 RD1561H9.SEQ A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C C C T C C A 200

GRVER51.SEQ T A A T T G T G G G T A C A A A A T G A A C G A T G T G G T G A G C A T T T G T 240
 GR6.SEQ T A A T T G T G G G T A C A A A A T G A A C G A T G T G G T G A G C A T T T G T 240
 GRVER5.SEQ T A A T T G T G G G T A C A A A A T G A A C G A T G T G G T G A G C A T T T G T 240
 GRVER4.SEQ T A A T T G T G G G T A C A A A A T G A A C G A T G T G G T G A G C A T T T G T 240
 GRVER3.SEQ T A A T T G T G G G T A C A A A A T G A A C G A T G T G G T G A G C A T C T G T 240
 GRVER2.SEQ T A A T T G C G G T T A C A A A A T G A A C G A T G T G G T C A G C A T T T G T 240
 GRVER1.SEQ T A A T T G C G G T T A C A A A A T G A A C G A T G T G G T C A G C A T T T G T 240
 YG81-6G1.SEQ C A A T T G T G G A T A C A A G A T G A A T G A T G T A G T G T C G A T C T G C 240
 RDVER1.SEQ C A A C T G T G G C T A T A A G A T G A A T G A C G T C G T G T C T A T C T G C 240
 RDVER2.SEQ C A A C T G T G G C T A T A A G A T G A A T G A C G T C G T G T C T A T C T G C 240
 RDVER3.SEQ T A A T T G C G G C T A C A A G A T G A A C G A C G T C G T C T C T A T T T G T 240
 RDVER4.SEQ T A A T T G T G G C T A C A A G A T G A A C G A C G T C G T C T C C A T T T G T 240
 RDVER5.SEQ C A A T T G T G G C T A C A A G A T G A A C G A C G T C G T T A G T A T C T G T 240
 RD7.SEQ C A A T T G T G G C T A C A A G A T G A A C G A C G T C G T T A G T A T C T G T 240
 RDVER51.SEQ C A A T T G T G G C T A C A A G A T G A A C G A C G T C G T T A G T A T C T G T 240
 RDVER52.SEQ C A A T T G T G G C T A C A A G A T G A A C G A C G T C G T T A G T A T C T G T 240
 RD1561H9.SEQ C A A T T G T G G C T A C A A G A T G A A C G A C G T C G T T A G T A T C T G T 240

Figure 2 (cont.)

GRVER51.SEQ	G	C	T	G	A	G	A	A	A	C	A	C	T	C	G	C	T	T	C	T	T	T	A	T	T	C	G	T	A	A	T	C	G	C	T	G	280		
GR6.SEQ	G	C	T	G	A	G	A	A	T	A	A	C	A	C	T	C	G	C	T	T	C	T	T	T	A	T	T	C	C	T	G	T	A	A	T	C	G	280	
GRVER5.SEQ	G	C	T	G	A	G	A	A	T	A	A	C	A	C	T	C	G	C	T	T	C	T	T	T	A	T	T	C	C	T	G	T	A	A	T	C	G	280	
GRVER4.SEQ	G	C	T	G	A	G	A	A	T	A	A	C	A	C	T	C	G	C	T	T	C	T	T	T	A	T	C	C	C	T	G	T	T	A	T	C	G	280	
GRVER3.SEQ	G	C	T	G	A	G	A	A	T	A	A	C	A	C	T	C	G	C	T	T	T	T	T	T	A	T	C	C	C	T	G	T	G	A	T	C	G	280	
GRVER2.SEQ	G	C	T	G	A	G	A	A	T	A	A	C	A	C	C	C	G	C	T	T	T	T	T	T	C	A	T	C	C	C	A	G	T	G	A	T	T	G	280
GRVER1.SEQ	G	C	T	G	A	G	A	A	T	A	A	C	A	C	C	C	G	C	T	T	T	T	T	T	C	A	T	C	C	C	A	G	T	G	A	T	T	G	280
YG81-6G1.SEQ	G	C	C	G	A	G	A	A	T	A	A	T	A	C	A	A	G	A	T	T	T	T	T	T	A	T	T	C	C	C	G	T	T	A	T	T	G	280	
RDVER1.SEQ	G	C	C	G	A	A	A	A	C	A	A	T	A	C	T	C	G	T	T	T	C	T	T	T	A	T	T	C	C	T	G	T	C	A	T	C	G	280	
RDVER2.SEQ	G	C	C	G	A	A	A	A	C	A	A	T	A	C	T	C	G	T	T	T	C	T	T	T	A	T	T	C	C	T	G	T	C	A	T	C	G	280	
RDVER3.SEQ	G	C	C	G	A	A	A	A	C	A	A	T	A	C	C	C	G	T	T	T	C	T	T	T	C	A	T	T	C	C	A	G	T	C	A	T	C	G	280
RDVER4.SEQ	G	C	A	G	A	A	A	A	C	A	A	T	A	C	C	C	G	T	T	T	C	T	T	T	C	A	T	T	C	C	A	G	T	C	A	T	C	G	280
RDVER5.SEQ	G	C	T	G	A	A	A	A	C	A	A	T	A	C	C	C	G	T	T	T	C	T	T	T	C	A	T	T	C	C	A	G	T	C	A	T	C	G	280
RD7.SEQ	G	C	T	G	A	A	A	A	C	A	A	T	A	C	C	C	G	T	T	T	C	T	T	T	C	A	T	T	C	C	A	G	T	C	A	T	C	G	280
RDVER51.SEQ	G	C	T	G	A	A	A	A	C	A	A	T	A	C	C	C	G	T	T	T	C	T	T	T	C	A	T	T	C	C	A	G	T	C	A	T	C	G	280
RDVER52.SEQ	G	C	T	G	A	A	A	A	C	A	A	T	A	C	C	C	G	T	T	T	C	T	T	T	C	A	T	T	C	C	A	G	T	C	A	T	C	G	280
RD1561H9.SEQ	G	C	T	G	A	A	A	A	C	A	A	T	A	C	C	C	G	T	T	T	C	T	T	T	C	A	T	T	C	C	A	G	T	C	A	T	C	G	280

GRVER51.SEQ	C	T	T	G	G	T	A	C	A	T	C	G	G	C	A	T	G	A	T	T	G	T	C	G	C	C	C	T	G	T	G	A	A	T	G	A	A	T	C	320
GR6.SEQ	C	T	T	G	G	T	A	C	A	T	C	G	G	C	A	T	G	A	T	T	G	T	C	G	C	C	C	T	G	T	G	A	A	T	G	A	A	T	C	320
GRVER5.SEQ	C	T	T	G	G	T	A	C	A	T	C	G	G	C	A	T	G	A	T	T	G	T	C	G	C	C	C	T	G	T	G	A	A	T	G	A	A	T	C	320
GRVER4.SEQ	C	T	T	G	G	T	A	C	A	T	C	G	G	C	A	T	G	A	T	T	G	T	C	G	C	C	C	T	G	T	G	A	A	T	G	A	A	T	C	320
GRVER3.SEQ	C	T	T	G	G	T	A	C	A	T	C	G	G	C	A	T	G	A	T	T	G	T	C	G	C	C	C	T	G	T	G	A	A	T	G	A	A	T	C	320
GRVER2.SEQ	C	T	T	G	G	T	A	C	A	T	C	G	G	C	A	T	G	A	T	T	G	T	C	G	C	C	C	T	G	T	G	A	A	T	G	A	A	T	C	320
GRVER1.SEQ	C	T	T	G	G	T	A	C	A	T	C	G	G	C	A	T	G	A	T	T	G	T	C	G	C	C	C	T	G	T	G	A	A	T	G	A	A	T	C	320
YG81-6G1.SEQ	C	T	T	G	G	T	A	T	A	T	T	G	G	T	A	T	G	A	T	T	G	T	A	G	C	A	C	C	T	G	T	T	A	A	T	G	A	A	G	320
RDVER1.SEQ	C	C	T	G	G	T	A	T	A	T	T	G	G	T	A	T	G	A	T	C	G	T	G	G	C	T	C	C	A	G	T	C	A	A	C	G	A	G	320	
RDVER2.SEQ	C	C	T	G	G	T	A	T	A	T	T	G	G	T	A	T	G	A	T	C	G	T	G	G	C	T	C	C	A	G	T	C	A	A	C	G	A	G	320	
RDVER3.SEQ	C	C	T	G	G	T	A	T	A	T	C	G	G	T	A	T	G	A	T	C	G	T	G	G	C	T	C	C	A	G	T	C	A	A	C	G	A	G	320	
RDVER4.SEQ	C	A	T	G	G	T	A	T	A	T	C	G	G	T	A	T	G	A	T	C	G	T	G	G	C	T	C	C	A	G	T	C	A	A	C	G	A	G	320	
RDVER5.SEQ	C	A	T	G	G	T	A	T	A	T	C	G	G	T	A	T	G	A	T	C	G	T	G	G	C	T	C	C	A	G	T	C	A	A	C	G	A	G	320	
RD7.SEQ	C	A	T	G	G	T	A	T	A	T	C	G	G	T	A	T	G	A	T	C	G	T	G	G	C	T	C	C	A	G	T	C	A	A	C	G	A	G	320	
RDVER51.SEQ	C	A	T	G	G	T	A	T	A	T	C	G	G	T	A	T	G	A	T	C	G	T	G	G	C	T	C	C	A	G	T	C	A	A	C	G	A	G	320	
RDVER52.SEQ	C	A	T	G	G	T	A	T	A	T	C	G	G	T	A	T	G	A	T	C	G	T	G	G	C	T	C	C	A	G	T	C	A	A	C	G	A	G	320	
RD1561H9.SEQ	C	A	T	G	G	T	A	T	A	T	C	G	G	T	A	T	G	A	T	C	G	T	G	G	C	T	C	C	A	G	T	C	A	A	C	G	A	G	320	

GRVER51.SEQ	T	T	A	C	A	T	C	C	C	A	G	A	T	G	A	G	C	T	G	T	G	T	A	A	G	G	T	T	A	T	G	G	G	T	A	T	T	A	G	C	360
GR6.SEQ	T	T	A	C	A	T	C	C	C	A	G	A	T	G	A	G	C	T	G	T	G	T	A	A	G	G	T	T	A	T	G	G	G	T	A	T	T	A	G	C	360
GRVER5.SEQ	T	T	A	C	A	T	C	C	C	A	G	A	T	G	A	G	C	T	G	T	G	T	A	A	G	G	T	T	A	T	G	G	G	T	A	T	T	A	G	C	360
GRVER4.SEQ	T	T	A	C	A	T	C	C	C	A	G	A	T	G	A	G	C	T	G	T	G	T	A	A	G	G	T	T	A	T	G	G	G	T	A	T	T	A	G	C	360
GRVER3.SEQ	T	T	A	C	A	T	C	C	C	A	G	A	T	G	A	G	T	T	G	T	G	T	A	A	G	G	T	G	A	T	G	G	G	T	A	T	T	A	G	C	360
GRVER2.SEQ	T	T	A	T	A	T	C	C	C	A	G	A	C	G	A	G	T	T	G	T	G	C	A	A	G	G	T	C	A	T	G	G	G	T	A	T	T	A	G	C	360
GRVER1.SEQ	T	T	A	T	A	T	C	C	C	A	G	A	C	G	A	G	T	T	G	T	G	C	A	A	G	G	T	C	A	T	G	G	G	T	A	T	T	A	G	C	360
YG81-6G1.SEQ	T	T	A	C	A	T	C	C	C	A	G	A	T	G	A	A	C	T	C	T	G	T	A	A	G	G	T	G	A	T	G	G	G	T	A	T	A	T	C	360	
RDVER1.SEQ	C	T	A	C	A	T	T	C	C	T	G	A	T	G	A	A	C	T	G	T	G	T	A	A	A	G	T	G	A	T	G	G	G	C	A	T	C	T	C	360	
RDVER2.SEQ	C	T	A	C	A	T	T	C	C	T	G	A	T	G	A	A	C	T	G	T	G	T	A	A	A	G	T	G	A	T	G	G	G	C	A	T	C	T	C	360	
RDVER3.SEQ	C	T	A	C	A	T	T	C	C	T	G	A	C	G	A	A	C	T	G	T	G	T	A	A	A	G	T	C	A	T	G	G	G	T	A	T	C	T	C	360	
RDVER4.SEQ	C	T	A	C	A	T	T	C	C	C	G	A	C	G	A	A	C	T	G	T	G	T	A	A	A	G	T	C	A	T	G	G	G	T	A	T	C	T	C	360	
RDVER5.SEQ	C	T	A	C	A	T	T	C	C	C	G	A	C	G	A	A	C	T	G	T	G	T	A	A	A	G	T	C	A	T	G	G	G	T	A	T	C	T	C	360	
RD7.SEQ	C	T	A	C	A	T	T	C	C	C	G	A	C	G	A	A	C	T	G	T	G	T	A	A	A	G	T	C	A	T	G	G	G	T	A	T	C	T	C	360	
RDVER51.SEQ	C	T	A	C	A	T	T	C	C	C	G	A	C	G	A	A	C	T	G	T	G	T	A	A	A	G	T	C	A	T	G	G	G	T	A	T	C	T	C	360	
RDVER52.SEQ	C	T	A	C	A	T	T	C	C	C	G	A	C	G	A	A	C	T	G	T	G	T	A	A	A	G	T	C	A	T	G	G	G	T	A	T	C	T	C	360	
RD1561H9.SEQ	C	T	A	C	A	T	T	C	C	C	G	A	C	G	A	A	C	T	G	T	G	T	A	A	A	G	T	C	A	T	G	G	G	T	A	T	C	T	C	360	

Figure 2 (cont.)

GRVER51.SEQ A A A C C T C A A A T C G T C T T T A C T A C C A A A A C A T C T T G A A T A 400
 GR6.SEQ A A A C C T C A A A T C G T C T T T A C T A C C A A A A A C A T C T T G A A T A 400
 GRVER5.SEQ A A A C C T C A A A T C G T C T T T A C T A C C A A A A A C A T C T T G A A T A 400
 GRVER4.SEQ A A A C C T C A A A T C G T C T T T A C T A C C A A A A A T A T C C T G A A T A 400
 GRVER3.SEQ A A A C C T C A A A T C G T C T T T A C T A C C A A A A A C A T C C T G A A T A 400
 GRVER2.SEQ A A A C C T C A A A T C G T G T T T A C T A C C A A G A A C A T T C T G A A T A 400
 GRVER1.SEQ A A A C C T C A A A T C G T G T T T A C T A C C A A G A A C A T T C T G A A T A 400
 YG81-6G1.SEQ A A A C C A C A A A T A G T T T T T A C G A C A A G A A C A T T T T A A A T A 400
 RDVER1.SEQ A A G C C A C A G A T T G T C T T C A C C A C T A A A A A T A T C T T G A A C A 400
 RDVER2.SEQ A A G C C A C A G A T T G T C T T C A C C A C T A A A A A T A T C T T G A A C A 400
 RDVER3.SEQ A A G C C A C A G A T T G T G T T C A C C A C T A A G A A T A T T T T G A A C A 400
 RDVER4.SEQ A A G C C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A 400
 RDVER5.SEQ A A G C C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A 400
 RD7.SEQ A A G C C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A 400
 RDVER51.SEQ A A G C C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A 400
 RDVER52.SEQ A A G C C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A 400
 RD1561H9.SEQ A A G C C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A 400

GRVER51.SEQ A G G T C T T G G A A G T C C A G T C T C G T A C T A A C T T C A T C A A A C G 440
 GR6.SEQ A G G T C T T G G A A G T C C A G T C T C G T A C T A A C T T C A T C A A A C G 440
 GRVER5.SEQ A G G T C T T G G A A G T C C A G T C T C G T A C T A A C T T C A T C A A A C G 440
 GRVER4.SEQ A G G T C T T G G A A G T C C A G T C T C G T A C T A A C T T C A T C A A A C G 440
 GRVER3.SEQ A G G T C T T G G A A G T C C A G T C T C G T A C T A A T T T C A T C A A A C G 440
 GRVER2.SEQ A G G T C T T G G A A G T G C A G T C T C G T A C T A A C T T C A T C A A G C G 440
 GRVER1.SEQ A A G T C T T G G A A G T G C A G T C T C G T A C T A A C T T C A T C A A G C G 440
 YG81-6G1.SEQ A G G T A T T G G A G G T A C A G A G C A G A A C T A A T T T C A T A A A A A G 440
 RDVER1.SEQ A G G T G C T G G A G G T C C A A A G C C G C A C C A A T T T T A T T A A A C G 440
 RDVER2.SEQ A A G T G C T G G A G G T C C A A A G C C G C A C C A A T T T T A T T A A A C G 440
 RDVER3.SEQ A A G T G C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G 440
 RDVER4.SEQ A A G T C C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G 440
 RDVER5.SEQ A A G T C C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G 440
 RD7.SEQ A A G T C C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G 440
 RDVER51.SEQ A A G T C C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G 440
 RDVER52.SEQ A A G T C C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G 440
 RD1561H9.SEQ A A G T C C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G 440

GRVER51.SEQ C A T C A T T A T T C T G G A T A C C G T C G A A A A C A T C C A C G G C T G T 480
 GR6.SEQ C A T C A T T A T T C T G G A T A C C G T C G A A A A C A T C C A C G G C T G T 480
 GRVER5.SEQ C A T C A T T A T T C T G G A T A C C G T C G A A A A C A T C C A C G G C T G T 480
 GRVER4.SEQ C A T C A T T A T T C T G G A T A C C G T C G A A A A C A T C C A T G G C T G T 480
 GRVER3.SEQ C A T T A T T A T T C T G G A T A C C G T C G A A A A C A T C C A C G G C T G T 480
 GRVER2.SEQ C A T T A T C A T T C T G G A T A C C G T C G A G A A T A T C C A C G G C T G T 480
 GRVER1.SEQ C A T T A T C A T T C T G G A T A C C G T C G A G A A T A T C C A C G G C T G T 480
 YG81-6G1.SEQ G A T C A T C A T A C T T G A T A C T G T A G A A A A C A T A C A C G G T T G T 480
 RDVER1.SEQ T A T C A T T A T C T T G G A C A C T G T G G A A A A C A T T C A T G G T T G C 480
 RDVER2.SEQ T A T C A T T A T C T T G G A C A C T G T G G A A A A C A T T C A T G G T T G C 480
 RDVER3.SEQ T A T C A T C A T C T T G G A C A C T G T G G A G A A T A T T C A T G G T T G C 480
 RDVER4.SEQ T A T C A T C A T C T T G G A C A C T G T G G A G A A T A T T C A C G G T T G C 480
 RDVER5.SEQ T A T C A T C A T C T T G G A C A C T G T G G A G A A T A T T C A C G G T T G C 480
 RD7.SEQ T A T C A T C A T C T T G G A C A C T G T G G A G A A T A T T C A C G G T T G C 480
 RDVER51.SEQ T A T C A T C A T C T T G G A C A C T G T G G A G A A T A T T C A C G G T T G C 480
 RDVER52.SEQ T A T C A T C A T C T T G G A C A C T G T G G A G A A T A T T C A C G G T T G C 480
 RD1561H9.SEQ T A T C A T C A T C T T G G A C A C T G T G G A G A A T A T T C A C G G T T G C 480

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Figure 2 (cont.)

GRVER51.SEQ G A G A G C C T C T A A C T T C A T C T C T C G T T A G C G A T G G T A 520
 GR6.SEQ G A G A G C C T C C C T A A C T T C A T C T C T C G T T A C A G C G A T G G T A 520
 GRVER5.SEQ G A G A G C C T C C C T A A C T T C A T C T C T C G T T A C A G C G A T G G T A 520
 GRVER4.SEQ G A G A G C C T G C C T A A C T T C A T C T C T C G T T A C A G C G A T G G T A 520
 GRVER3.SEQ G A G A G C T T G C C T A A C T T T A T C T C T C G T T A C A G C G A T G G T A 520
 GRVER2.SEQ G A G A G C T T G C C A A A C T T T A T T T C T C G T T A T A G C G A C G G T A 520
 GRVER1.SEQ G A A A G C T T G C C A A A C T T T A T T T C T C G T T A T A G C G A C G G T A 520
 YG81-6G1.SEQ G A A A G T C T T C C C A A T T T T A T T T C T C G T T A T T C G G A T G G A A 520
 RDVER1.SEQ G A G T C T C T G C C T A A T T T C A T C A G C C G C T A C T C T G A T G G C A 520
 RDVER2.SEQ G A A T C T C T G C C T A A T T T C A T C A G C C G C T A C T C T G A T G G C A 520
 RDVER3.SEQ G A A T C T C T G C C T A A T T T C A T T A G C C G C T A T T C T G A C G G C A 520
 RDVER4.SEQ G A A T C T T T G C C T A A T T T T A T T A G C C G C T A T T C A G A C G G A A 520
 RDVER5.SEQ G A A T C T T T G C C T A A T T T C A T C T C T C G C T A T T C A G A C G G C A 520
 RD7.SEQ G A A T C T T T G C C T A A T T T C A T C T C T C G C T A T T C A G A C G G C A 520
 RDVER51.SEQ G A A T C T T T G C C T A A T T T C A T C T C T C G C T A T T C A G A C G G C A 520
 RDVER52.SEQ G A A T C T T T G C C T A A T T T C A T C T C T C G C T A T T C A G A C G G C A 520
 RD1561H9.SEQ G A A T C T T T G C C T A A T T T C A T C T C T C G C T A T T C A G A C G G C A 520

GRVER51.SEQ A T A T C G C T A A T T T C A A G C C C T T G C A T T T T G A T C C A G T C G A 560
 GR6.SEQ A T A T C G C T A A T T T C A A G C C C T T G C A T T T T G A T C C A G T C G A 560
 GRVER5.SEQ A T A T C G C T A A T T T C A A G C C C T T G C A T T T T G A T C C A G T C G A 560
 GRVER4.SEQ A T A T C G C T A A T T T C A A A C C A C T G C A T T T T G A T C C A G T C G A 560
 GRVER3.SEQ A T A T C G C T A A T T T C A A G C C A C T G C A T T T T G A T C C A G T C G A 560
 GRVER2.SEQ A T A T C G C T A A C T T C A A G C C T C T G C A T T T T G A T C C A G T G G A 560
 GRVER1.SEQ A T A T C G C T A A C T T C A A G C C T C T G C A T T T T G A T C C A G T G G A 560
 YG81-6G1.SEQ A T A T T G C C A A C T T C A A A C C T T T A C A T T T C G A T C C T G T T G A 560
 RDVER1.SEQ A C A T T G C C A A T T T T A A A C C A T T G C A C T T C G A C C C T G T C G A 560
 RDVER2.SEQ A C A T T G C C A A T T T T A A A C C A T T G C A C T T C G A C C C T G T C G A 560
 RDVER3.SEQ A C A T C G C C A A C T T T A A A C C T T T G C A T T T C G A C C C T G T G G A 560
 RDVER4.SEQ A C A T C G C C A A C T T T A A A G C C T C T C A T T T C G A C C C T G T G G A 560
 RDVER5.SEQ A C A T C G C A A A C T T T A A A C C A C T C C A C T T C G A C C C T G T G G A 560
 RD7.SEQ A C A T C G C A A A C T T T A A A C C A C T C C A C T T C G A C C C T G T G G A 560
 RDVER51.SEQ A C A T C G C A A A C T T T A A A C C A C T C C A C T T C G A C C C T G T G G A 560
 RDVER52.SEQ A C A T C G C A A A C T T T A A A C C A C T C C A C T T C G A C C C T G T G G A 560
 RD1561H9.SEQ A C A T C G C A A A C T T T A A A C C A C T C C A C T T C G A C C C T G T G G A 560

GRVER51.SEQ G C A A G T G G C C G C T A T T T T G T G C T C C T C C G G C A C C A C T G G T 600
 GR6.SEQ G C A A G T G G C C G C T A T T T T G T G C T C C T C C G G C A C C A C T G G T 600
 GRVER5.SEQ G C A A G T G G C C G C T A T T T T G T G C T C C T C C G G C A C C A C T G G T 600
 GRVER4.SEQ G C A A G T G G C C G C T A T T T T G T G C T C T T C C G G C A C C A C T G G T 600
 GRVER3.SEQ G C A G G T C G C G C C A T T T T G T G C T C T T C T G G C A C C A C T G G T 600
 GRVER2.SEQ G C A A G T C G C G C C T A T T T T G T G C T C T A G C G G C A C C A C C G G T 600
 GRVER1.SEQ G C A A G T C G C C G C T A T T T T G T G C T C T A G C G G C A C T A C C G G T 600
 YG81-6G1.SEQ G C A A G T G G C A G C T A T C T T A T G T T C G T C A G G C A C T A C T G G A 600
 RDVER1.SEQ A C A G G T G G C T G C C A T C C T G T G T A G C T C T G G T A C T A C T G G C 600
 RDVER2.SEQ A C A G G T G G C T G C C A T C C T G T G T A G C T C T G G T A C T A C T G G C 600
 RDVER3.SEQ A C A A G T G G C T G C T A T C C T G T G T A G C A G C G G T A C T A C T G G C 600
 RDVER4.SEQ A C A A G T T G C T G C A A T C C T G T G T A G C A G C G G T A C T A C T G G A 600
 RDVER5.SEQ A C A A G T T G C A G C C A T T C T G T G T A G C A G C G G T A C T A C T G G A 600
 RD7.SEQ A C A A G T T G C A G C C A T T C T G T G T A G C A G C G G T A C T A C T G G A 600
 RDVER51.SEQ A C A A G T T G C A G C C A T T C T G T G T A G C A G C G G T A C T A C T G G A 600
 RDVER52.SEQ A C A A G T T G C A G C C A T T C T G T G T A G C A G C G G T A C T A C T G G A 600
 RD1561H9.SEQ A C A A G T T G C A G C C A T T C T G T G T A G C A G C G G T A C T A C T G G A 600

Figure 2 (cont.)

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GRVER51.SEQ T T G C C T A A A G T G T C A T G C A G A C T C A C C A A A T A T C T G T G 640
GR6.SEQ      T T G C C T A A A G T G T C A T G C A G A C T C A C C A G A A T A T C T G T G 640
GRVER5.SEQ   T T G C C T A A A G T G T C A T G C A G A C T C A C C A G A A T A T C T G T G 640
GRVER4.SEQ   T T G C C T A A A G T G T C A T G C A G A C T C A C C A G A A T A T C T G T G 640
GRVER3.SEQ   T T G C C T A A A G T G T C A T G C A G A C T C A C C A G A A T A T C T G T G 640
GRVER2.SEQ   C T G C C T A A A G G C G T G A T G C A G A C T C A C C A A A A T A T C T G T G 640
GRVER1.SEQ   C T G C C T A A A G G C G T G A T G C A G A C T C A C C A A A A T A T C T G T G 640
YG81-6G1.SEQ T T A C C G A A A G T G T A A T G C A A A C T C A C C A A A A T A T T T G T G 640
RDVER1.SEQ   T T G C C A A A G G T G T C A T G C A A A C C C A T C A G A A C A T T T G C G 640
RDVER2.SEQ   T T G C C A A A G G T G T C A T G C A A A C C C A T C A G A A C A T T T G C G 640
RDVER3.SEQ   C T C C C A A A G G G C G T C A T G C A G A C C C A T C A A A A C A T T T G C G 640
RDVER4.SEQ   C T C C C A A A G G G A G T C A T G C A G A C C C A T C A A A A C A T T T G C G 640
RDVER5.SEQ   C T C C C A A A G G G A G T C A T G C A G A C C C A T C A A A A C A T T T G C G 640
RD7.SEQ      C T C C C A A A G G G A G T C A T G C A G A C C C A T C A A A A C A T T T G C G 640
RDVER51.SEQ  C T C C C A A A G G G A G T C A T G C A G A C C C A T C A A A A C A T T T G C G 640
RDVER52.SEQ  C T C C C A A A G G G A G T C A T G C A G A C C C A T C A A A A C A T T T G C G 640
RD1561H9.SEQ C T C C C A A A G G G A G T C A T G C A G A C C C A T C A A A A C A T T T G C G 640

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GRVER51.SEQ T G C G T T T G A T C C A C G C T C T C G A C C C T C G T G T G G G T A C T C A 680
GR6.SEQ      T G C G T T T G A T C C A C G C T C T C G A C C C T C G T G T G G G T A C T C A 680
GRVER5.SEQ   T G C G T T T G A T C C A C G C T C T C G A C C C T C G T G T G G G T A C T C A 680
GRVER4.SEQ   T G C G T T T G A T C C A C G C T C T C G A C C C T C G T G T G G G T A C T C A 680
GRVER3.SEQ   T G C G C T T G A T C C A C G C C C T C G A C C C T C G T G T G G G T A C T C A 680
GRVER2.SEQ   T C C G C T T G A T T C A T G C C C T G G A C C C A C G T G T G G G T A C T C A 680
GRVER1.SEQ   T C C G C T T G A T T C A T G C C C T G G A C C C A C G T G T G G G T A C C C A 680
YG81-6G1.SEQ T C C G A C T T A T A C A T G C T T T A G A C C C C A G G G C A G G A A C G C A 680
RDVER1.SEQ   T G C G T C T G A T C C A C G C T C T C G A T C C T C G C T A C G G C A C T C A 680
RDVER2.SEQ   T G C G T C T G A T C C A C G C T C T C G A T C C T C G C T A C G G C A C C C A 680
RDVER3.SEQ   T G C G T C T G A T C C A T G C T C T C G A T C C A C G C T A C G G C A C T C A 680
RDVER4.SEQ   T G C G T C T G A T C C A T G C T C T C G A T C C A C G C T A C G G C A C T C A 680
RDVER5.SEQ   T G C G T C T G A T C C A T G C T C T C G A T C C A C G C T A C G G C A C T C A 680
RD7.SEQ      T G C G T C T G A T C C A T G C T C T C G A T C C A C G C T A C G G C A C T C A 680
RDVER51.SEQ  T G C G T C T G A T C C A T G C T C T C G A T C C A C G C T A C G G C A C T C A 680
RDVER52.SEQ  T G C G T C T G A T C C A T G C T C T C G A T C C A C G C T A C G G C A C T C A 680
RD1561H9.SEQ T G C G T C T G A T C C A T G C T C T C G A T C C A C G C T A C G G C A C T C A 680

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GRVER51.SEQ A T T G A T C C C T G G C G T G A C T G T G C T G G T G T A T C T G C C T T T C 720
GR6.SEQ      A T T G A T C C C T G G C G T G A C T G T G C T G G T G T A T C T G C C T T T C 720
GRVER5.SEQ   A T T G A T C C C T G G C G T G A C T G T G C T G G T G T A T C T G C C T T T C 720
GRVER4.SEQ   A T T G A T C C C T G G C G T G A C T G T G C T G G T G T A T C T G C C T T T C 720
GRVER3.SEQ   A T T G A T C C C T G G C G T G A C T G T G C T G G T G T A T T T G C C T T T C 720
GRVER2.SEQ   G T T G A T C C C T G G C G T G A C T G T C C T G G T G T A C T T G C C A T T C 720
GRVER1.SEQ   G T T G A T C C C T G G C G T G A C T G T C C T G G T G T A C T T G C C A T T C 720
YG81-6G1.SEQ A C T T A T T C C T G G T G T G A C A G T C T T A G T A T A T C T G C C T T T T 720
RDVER1.SEQ   A C T G A T T C C A G G T G T C A C C G T G T T G G T C T A T C T G C C T T T T 720
RDVER2.SEQ   A C T G A T T C C T G G T G T C A C C G T G T T G G T C T A T C T G C C T T T T 720
RDVER3.SEQ   G C T G A T T C C T G G T G T C A C C G T C T T G G T C T A C C T G C C T T T C 720
RDVER4.SEQ   G C T G A T T C C T G G T G T C A C C G T C T T G G T C T A C T T G C C T T T C 720
RDVER5.SEQ   G C T G A T T C C T G G T G T C A C C G T C T T G G T C T A C T T G C C T T T C 720
RD7.SEQ      G C T G A T T C C T G G T G T C A C C G T C T T G G T C T A C T T G C C T T T C 720
RDVER51.SEQ  G C T G A T T C C T G G T G T C A C C G T C T T G G T C T A C T T G C C T T T C 720
RDVER52.SEQ  G C T G A T T C C T G G T G T C A C C G T C T T G G T C T A C T T G C C T T T C 720
RD1561H9.SEQ G C T G A T T C C T G G T G T C A C C G T C T T G G T C T A C T T G C C T T T C 720

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Figure 2 (cont.)

GRVER51.SEQ	T	T	T	C	A	C	G	C	T	T	T	G	G	T	T	T	C	T	C	T	A	T	T	A	C	C	T	G	G	G	C	T	A	T	T	T	C	A	760				
GR6.SEQ	T	T	T	C	A	C	G	C	C	T	T	T	G	G	T	T	T	C	T	C	T	A	T	T	A	C	C	T	G	G	G	C	T	A	T	T	T	C	A	760			
GRVER5.SEQ	T	T	T	C	A	C	G	C	C	T	T	T	G	G	T	T	T	C	T	C	T	A	T	T	A	C	C	T	G	G	G	C	T	A	T	T	T	C	A	760			
GRVER4.SEQ	T	T	T	C	A	C	G	C	C	T	T	T	G	G	T	T	T	T	C	T	A	T	T	A	C	C	C	T	G	G	G	C	T	A	T	T	T	C	A	760			
GRVER3.SEQ	T	T	T	C	A	C	G	C	C	T	T	T	G	G	T	T	T	T	T	C	T	A	T	T	A	C	C	C	T	G	G	G	C	T	A	T	T	T	C	A	760		
GRVER2.SEQ	T	T	T	C	A	C	G	C	C	T	T	C	G	G	T	T	T	T	T	C	T	A	T	T	A	C	C	C	T	G	G	G	C	T	A	T	T	T	C	A	760		
GRVER1.SEQ	T	T	T	C	A	C	G	C	C	T	T	C	G	G	T	T	T	T	T	C	T	A	T	T	A	C	C	C	T	G	G	G	C	T	A	T	T	T	C	A	760		
YG81-6G1.SEQ	T	T	C	C	A	T	G	C	T	T	T	T	G	G	G	T	T	C	T	C	T	A	T	A	A	C	C	T	T	G	G	G	A	T	A	C	T	T	C	A	760		
RDVER1.SEQ	T	T	C	C	A	T	G	C	T	T	T	T	G	G	C	T	T	C	C	A	C	A	T	C	A	C	T	T	T	G	G	G	T	T	A	C	T	T	T	A	760		
RDVER2.SEQ	T	T	C	C	A	T	G	C	T	T	T	T	G	G	C	T	T	C	C	A	C	A	T	C	A	C	T	T	T	G	G	G	T	T	A	C	T	T	T	A	760		
RDVER3.SEQ	T	T	C	C	A	T	G	C	T	T	T	C	G	G	C	T	T	C	C	A	C	A	T	T	A	C	T	T	T	G	G	G	T	T	A	C	T	T	T	A	760		
RDVER4.SEQ	T	T	C	C	A	T	G	C	T	T	T	C	G	G	C	T	T	C	C	A	T	A	T	T	A	C	T	T	T	G	G	G	T	T	A	C	T	T	T	A	760		
RDVER5.SEQ	T	T	C	C	A	T	G	C	T	T	T	C	G	G	C	T	T	T	C	A	T	A	T	T	A	C	T	T	T	G	G	G	T	T	A	C	T	T	T	A	760		
RD7.SEQ	T	T	C	C	A	T	G	C	T	T	T	C	G	G	C	T	T	T	C	A	T	A	T	T	A	C	T	T	T	G	G	G	T	T	A	C	T	T	T	A	760		
RDVER51.SEQ	T	T	C	C	A	T	G	C	T	T	T	C	G	G	C	T	T	T	C	A	T	A	T	T	A	C	T	T	T	G	G	G	T	T	A	C	T	T	T	A	760		
RDVER52.SEQ	T	T	C	C	A	T	G	C	T	T	T	C	G	G	C	T	T	T	C	A	T	A	T	T	A	C	T	T	T	G	G	G	T	T	A	C	T	T	T	A	760		
RD1561H9.SEQ	T	T	C	C	A	T	G	C	T	T	T	C	G	G	C	T	T	T	C	A	T	A	T	T	A	C	T	T	T	G	G	G	T	T	A	C	T	T	T	A	760		
GRVER51.SEQ	T	G	G	T	C	G	G	C	T	T	G	C	G	T	G	T	C	A	T	C	A	T	G	T	T	T	C	G	T	C	G	C	T	T	C	G	A	C	C	A	800		
GR6.SEQ	T	G	G	T	C	G	G	C	T	T	G	C	G	T	G	T	C	A	T	C	A	T	G	T	T	T	T	C	G	T	C	G	C	T	T	C	G	A	C	C	A	800	
GRVER5.SEQ	T	G	G	T	C	G	G	C	T	T	G	C	G	T	G	T	C	A	T	C	A	T	G	T	T	T	T	C	G	T	C	G	C	T	T	C	G	A	C	C	A	800	
GRVER4.SEQ	T	G	G	T	C	G	G	C	T	T	G	C	G	T	G	T	C	A	T	C	A	T	G	T	T	T	T	C	G	T	C	G	C	T	T	C	G	A	C	C	A	800	
GRVER3.SEQ	T	G	G	T	C	G	G	C	T	T	G	C	G	T	G	T	G	A	T	C	A	T	G	T	T	T	T	C	G	T	C	G	C	T	T	C	G	A	C	C	A	800	
GRVER2.SEQ	T	G	G	T	C	G	G	T	T	T	G	C	G	C	G	T	G	A	T	C	A	T	G	T	T	T	T	C	G	T	C	G	C	T	T	C	G	A	T	C	A	800	
GRVER1.SEQ	T	G	G	T	C	G	G	T	T	T	G	C	G	C	G	T	G	A	T	C	A	T	G	T	T	T	T	C	G	T	C	G	C	T	T	C	G	A	T	C	A	800	
YG81-6G1.SEQ	T	G	G	T	G	G	G	T	C	T	T	C	G	T	G	T	T	A	T	C	A	T	G	T	T	T	T	C	A	G	A	C	G	A	T	T	T	G	A	T	C	A	800
RDVER1.SEQ	T	G	G	T	G	G	G	C	C	T	G	C	G	T	G	T	C	A	T	T	A	T	G	T	T	T	T	C	G	C	C	G	T	T	T	T	G	A	C	C	A	800	
RDVER2.SEQ	T	G	G	T	G	G	G	C	C	T	G	C	G	T	G	T	C	A	T	T	A	T	G	T	T	T	T	C	G	C	C	G	T	T	T	T	G	A	C	C	A	800	
RDVER3.SEQ	T	G	G	T	C	G	G	T	C	T	G	C	G	T	G	T	C	A	T	T	A	T	G	T	T	T	T	C	G	C	C	G	T	T	T	T	G	A	T	C	A	800	
RDVER4.SEQ	T	G	G	T	C	G	G	T	C	T	G	C	G	T	G	T	G	A	T	T	A	T	G	T	T	T	T	C	G	C	C	G	T	T	T	T	G	A	T	C	A	800	
RDVER5.SEQ	T	G	G	T	C	G	G	T	C	T	C	C	G	C	G	T	G	A	T	T	A	T	G	T	T	T	T	C	G	C	C	G	T	T	T	T	G	A	T	C	A	800	
RD7.SEQ	T	G	G	T	C	G	G	T	C	T	C	C	G	C	G	T	G	A	T	T	A	T	G	T	T	T	T	C	G	C	C	G	T	T	T	T	G	A	T	C	A	800	
RDVER51.SEQ	T	G	G	T	C	G	G	T	C	T	C	C	G	C	G	T	G	A	T	T	A	T	G	T	T	T	T	C	G	C	C	G	T	T	T	T	G	A	T	C	A	800	
RDVER52.SEQ	T	G	G	T	C	G	G	T	C	T	C	C	G	C	G	T	G	A	T	T	A	T	G	T	T	T	T	C	G	C	C	G	T	T	T	T	G	A	T	C	A	800	
RD1561H9.SEQ	T	G	G	T	C	G	G	T	C	T	C	C	G	C	G	T	G	A	T	T	A	T	G	T	T	T	T	C	G	C	C	G	T	T	T	T	G	A	T	C	A	800	
GRVER51.SEQ	A	G	A	A	G	C	C	T	T	C	T	T	G	A	A	G	G	C	T	A	T	T	C	A	A	G	A	C	T	A	C	G	A	G	G	T	G	C	G	T	840		
GR6.SEQ	A	G	A	A	G	C	C	T	T	C	T	T	G	A	A	G	G	C	T	A	T	T	C	A	A	G	A	C	T	A	C	G	A	G	G	T	G	C	G	T	840		
GRVER5.SEQ	A	G	A	A	G	C	C	T	T	C	T	T	G	A	A	G	G	C	T	A	T	T	C	A	A	G	A	C	T	A	C	G	A	G	G	T	G	C	G	T	840		
GRVER4.SEQ	A	G	A	A	G	C	C	T	T	C	T	T	G	A	A	G	G	C	T	A	T	T	C	A	A	G	A	C	T	A	C	G	A	G	G	T	G	C	G	T	840		
GRVER3.SEQ	A	G	A	A	G	C	C	T	T	C	T	T	G	A	A	G	G	C	T	A	T	T	C	A	A	G	A	C	T	A	C	G	A	G	G	T	G	C	G	T	840		
GRVER2.SEQ	A	G	A	A	G	C	C	T	T	T	C	T	G	A	A	G	G	C	C	A	T	T	C	A	A	G	A	C	T	A	C	G	A	G	G	T	C	C	G	T	840		
GRVER1.SEQ	A	G	A	A	G	C	T	T	T	T	C	T	G	A	A	G	G	C	C	A	T	T	C	A	G	G	A	C	T	A	C	G	A	G	G	T	C	C	G	T	840		
YG81-6G1.SEQ	A	G	A	A	G	C	A	T	T	T	C	T	A	A	A	G	C	T	A	T	T	C	A	G	G	A	T	T	A	T	G	A	A	G	T	T	C	G	A	840			
RDVER1.SEQ	G	G	A	G	G	C	C	T	T	C	T	T	G	A	A	G	C	T	A	T	C	C	A	A	G	A	T	T	A	T	G	A	A	G	T	G	C	G	C	840			
RDVER2.SEQ	G	G	A	G	G	C	T	T	T	C	T	T	G	A	A	G	C	T	A	T	C	C	A	A	G	A	T	T	A	T	G	A	A	G	T	G	C	G	C	840			
RDVER3.SEQ	G	G	A	G	G	C	T	T	T	T	T	T	G	A	A	G	C	C	A	T	C	C	A	A	G	A	T	T	A	T	G	A	A	G	T	C	C	G	C	840			
RDVER4.SEQ	G	G	A	G	G	C	T	T	T	C	T	T	G	A	A	G	C	C	A	T	C	C	A	A	G	A	T	T	A	T	G	A	A	G	T	C	C	G	C	840			
RDVER5.SEQ	G	G	A	G	G	C	T	T	T	C	T	T	G	A	A	G	C	C	A	T	C	C	A	A	G	A	T	T	A	T	G	A	A	G	T	C	C	G	C	840			
RD7.SEQ	G	G	A	G	G	C	T	T	T	C	T	T	G	A	A	G	C	C	A	T	C	C	A	A	G	A	T	T	A	T	G	A	A	G	T	C	C	G	C	840			
RDVER51.SEQ	G	G	A	G	G	C	T	T	T	C	T	T	G	A	A	G	C	C	A	T	C	C	A	A	G	A	T	T	A	T	G	A	A	G	T	C	C	G	C	840			
RDVER52.SEQ	G	G	A	G	G	C	T	T	T	C	T	T	G	A	A	G	C	C	A	T	C	C	A	A	G	A	T	T	A	T	G	A	A	G	T	C	C	G	C	840			
RD1561H9.SEQ	G	G	A	G	G	C	T	T	T	C	T	T	G	A	A	G	C	C	A	T	C	C	A	A	G	A	T	T	A	T	G	A	A	G	T	C	C	G	C	840			

Figure 2 (cont.)

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GRVER51.SEQ T C C G T G A T C A A C G T C C C T T C A G T C A T T T T G T T C C T G A G C A 880
GR6.SEQ      T C C G T G A T C A A C G T C C C T T C A G T C A T T T T G T T C C T G A G C A 880
GRVER5.SEQ   T C C G T G A T C A A C G T C C C T T C A G T C A T T T T G T T C C T G A G C A 880
GRVER4.SEQ   T C T G T C A T C A A T G T C C C T T C A G T C A T T T T G T T C C T G A G C A 880
GRVER3.SEQ   T C T G T G A T C A A T G T C C C A T C T G T C A T T T T G T T C C T G A G C A 880
GRVER2.SEQ   A G C G T G A T C A A C G T C C C T T C T G T G A T T T T G T T C C T G A G C A 880
GRVER1.SEQ   A G C G T G A T C A A C G T C C C T T C T G T G A T T T T G T T C C T G A G C A 880
YG81-6G1.SEQ A G T G T A A T T A A C G T T C C A T C A G T A A T A T T G T T C T T A T C G A 880
RDVER1.SEQ   T C T G T C A T T A A T G T G C C A A G C G T C A T C C T G T T T T T G T C T A 880
RDVER2.SEQ   T C T G T C A T T A A T G T G C C A A G C G T C A T C C T G T T T T T G T C T A 880
RDVER3.SEQ   A G C G T C A T T A A C G T G C C T A G C G T G A T C C T G T T T T T G T C T A 880
RDVER4.SEQ   A G T G T C A T C A A C G T G C C T A G C G T G A T C C T G T T T T T G T C T A 880
RDVER5.SEQ   A G T G T C A T C A A C G T G C C T A G C G T G A T C C T G T T T T T G T C T A 880
RD7.SEQ      A G T G T C A T C A A C G T G C C T A G C G T G A T C C T G T T T T T G T C T A 880
RDVER51.SEQ  A G T G T C A T C A A C G T G C C T A G C G T G A T C C T G T T T T T G T C T A 880
RDVER52.SEQ  A G T G T C A T C A A C G T G C C T A G C G T G A T C C T G T T T T T G T C T A 880
RD1561H9.SEQ A G T G T C A T C A A C G T G C C T A G C G T G A T C C T G T T T T T G T C T A 880
  
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GRVER51.SEQ A A T C T C C T T T G G T T G A C A A G T A T G A T C T G A G C A G C T T G C G 920
GR6.SEQ      A A T C T C C T T T G G T T G A C A A G T A T G A T C T G A G C A G C T T G C G 920
GRVER5.SEQ   A A T C T C C T T T G G T T G A C A A G T A T G A T C T G A G C A G C T T G C G 920
GRVER4.SEQ   A A T C T C C T T T G G T T G A C A A G T A T G A T C T G A G C A G C T T G C G 920
GRVER3.SEQ   A A T C T C C T T T G G T T G A C A A G T A T G A T C T G A G C A G C T T G C G 920
GRVER2.SEQ   A A T C T C C A T T G G T C G A T A A G T A T G A C C T G A G C A G C T T G C G 920
GRVER1.SEQ   A A T C T C C A T T G G T C G A T A A G T A T G A C C T G A G C A G C T T T G C G 920
YG81-6G1.SEQ A A A G T C C T T T G G T T G A C A A A T A C G A T T T A T C A A G T T T A A G 920
RDVER1.SEQ   A G A G C C C T C T G G T G G A C A A A T A C G A T T T G T C T A G C C T G C G 920
RDVER2.SEQ   A G A G C C C T C T G G T G G A C A A A T A C G A T T T G T C T T C T C T G C G 920
RDVER3.SEQ   A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C C C T G C G 920
RDVER4.SEQ   A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C A C T G C G 920
RDVER5.SEQ   A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C A C T G C G 920
RD7.SEQ      A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C A C T G C G 920
RDVER51.SEQ  A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C A C T G C G 920
RDVER52.SEQ  A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C A C T G C G 920
RD1561H9.SEQ A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C A C T G C G 920
  
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GRVER51.SEQ T G A G C T G T G C T G T G G C G C T G C T C C T T T G G C C A A A G A A G T G 960
GR6.SEQ      T G A G C T G T G C T G T G G C G C T G C T C C T T T G G C C A A A G A A G T G 960
GRVER5.SEQ   T G A G C T G T G C T G T G G C G C T G C T C C T T T G G C C A A A G A A G T G 960
GRVER4.SEQ   T G A G C T G T G C T G T G G C G C T G C T C C T T T G G C C A A A G A A G T G 960
GRVER3.SEQ   T G A A C T G T G C T G T G G C G C T G C T C C T T T G G C C A A A G A A G T G 960
GRVER2.SEQ   C G A A C T G T G C T G T G G C G C T G C C C T T T G G C T A A A G A G G T G 960
GRVER1.SEQ   C G A A C T G T G C T G T G G C G C T G C C C T T T G G C T A A A G A G G T G 960
YG81-6G1.SEQ G G A A T T G T G T T G C G G T G C G G C A C C A T T A G C A A A A G A A G T T 960
RDVER1.SEQ   T G A G T T G T G T T G C G G T G C C G C T C C A C T G G C C A A G G A A G T C 960
RDVER2.SEQ   T G A G T T G T G T T G C G G T G C C G C T C C A C T G G C C A A G G A A G T C 960
RDVER3.SEQ   T G A G T T G T G T T G C G G T G C C G C C C A C T G G C T A A G G A G G T C 960
RDVER4.SEQ   T G A A T T G T G T T G C G G T G C C G C T C C A C T G G C T A A G G A G G T C 960
RDVER5.SEQ   T G A A T T G T G T T G C G G T G C C G C T C C A C T G G C T A A G G A G G T C 960
RD7.SEQ      T G A A T T G T G T T G C G G T G C C G C T C C A C T G G C T A A G G A G G T C 960
RDVER51.SEQ  T G A A T T G T G T T G C G G T G C C G C T C C A C T G G C T A A G G A G G T C 960
RDVER52.SEQ  T G A A T T G T G T T G C G G T G C C G C T C C A C T G G C T A A G G A G G T C 960
RD1561H9.SEQ T G A A T T G T G T T G C G G T G C C G C T C C A C T G G C T A A G G A G G T C 960
  
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Figure 2 (cont.)

GRVER51.SEQ	G	C	C	G	A	G	G	T	C	G	C	T	G	C	T	A	A	G	C	G	T	C	T	G	A	A	C	C	C	T	G	G	T	A	T	C	C	1000			
GR6.SEQ	G	C	C	G	A	G	G	T	C	G	C	T	G	C	T	A	A	G	C	G	T	C	T	G	A	A	C	C	C	T	G	G	T	A	T	C	C	1000			
GRVER5.SEQ	G	C	C	G	A	G	G	T	C	G	C	T	G	C	T	A	A	G	C	G	T	C	T	G	A	A	C	C	C	T	G	G	T	A	T	C	C	1000			
GRVER4.SEQ	G	C	C	G	A	G	G	T	C	G	C	T	G	C	T	A	A	G	C	G	T	C	T	G	A	A	C	C	C	T	G	G	T	A	T	C	C	1000			
GRVER3.SEQ	G	C	C	G	A	G	G	T	C	G	C	T	G	C	T	A	A	G	C	G	T	C	T	G	A	A	C	C	T	C	C	T	G	G	T	A	T	C	C	1000	
GRVER2.SEQ	G	C	C	G	A	A	G	T	C	G	C	T	G	C	C	A	A	G	C	G	T	C	T	G	A	A	T	T	T	G	C	C	A	G	G	T	A	T	C	C	1000
GRVER1.SEQ	G	C	C	G	A	A	G	T	C	G	C	T	G	C	C	A	A	G	C	G	T	C	T	G	A	A	T	T	T	G	C	C	A	G	G	T	A	T	C	C	1000
YG81-6G1.SEQ	G	C	T	G	A	G	G	T	T	G	C	A	G	C	A	A	A	A	C	G	A	T	T	A	A	A	C	T	T	G	C	C	A	G	G	A	A	T	T	C	1000
RDVER1.SEQ	G	C	T	G	A	G	G	T	G	G	C	C	G	C	T	A	A	A	C	G	C	T	T	G	A	A	C	C	T	G	C	C	T	G	G	C	A	T	T	C	1000
RDVER2.SEQ	G	C	T	G	A	G	G	T	G	G	C	C	G	C	T	A	A	A	C	G	C	T	T	G	A	A	C	C	T	G	C	C	T	G	G	C	A	T	T	C	1000
RDVER3.SEQ	G	C	T	G	A	A	G	T	G	G	C	C	G	C	C	A	A	A	C	G	C	T	T	G	A	A	T	C	T	G	C	C	A	G	G	C	A	T	T	C	1000
RDVER4.SEQ	G	C	T	G	A	A	G	T	G	G	C	C	G	C	C	A	A	A	C	G	C	T	T	G	A	A	T	C	T	G	C	C	C	G	G	C	A	T	T	C	1000
RDVER5.SEQ	G	C	T	G	A	A	G	T	G	G	C	C	G	C	C	A	A	A	C	G	C	T	T	G	A	A	T	C	T	T	C	A	G	G	G	A	T	T	C	1000	
RD7.SEQ	G	C	T	G	A	A	G	T	G	G	C	C	G	C	C	A	A	A	C	G	C	T	T	G	A	A	T	C	T	T	C	A	G	G	G	A	T	T	C	1000	
RDVER51.SEQ	G	C	T	G	A	A	G	T	G	G	C	C	G	C	C	A	A	A	C	G	C	T	T	G	A	A	T	C	T	T	C	A	G	G	G	A	T	T	C	1000	
RDVER52.SEQ	G	C	T	G	A	A	G	T	G	G	C	C	G	C	C	A	A	A	C	G	C	T	T	G	A	A	T	C	T	T	C	A	G	G	G	A	T	T	C	1000	
RD1561H9.SEQ	G	C	T	G	A	A	G	T	G	G	C	C	G	C	C	A	A	A	C	G	C	T	T	G	A	A	T	C	T	T	C	A	G	G	G	A	T	T	C	1000	

GRVER51.SEQ	G	C	T	G	C	G	G	T	T	T	T	G	G	T	T	T	G	A	C	T	G	A	G	A	G	C	A	C	T	T	C	T	G	C	T	A	A	C	A	T	1040
GR6.SEQ	G	C	T	G	C	G	G	T	T	T	T	G	G	T	T	T	G	A	C	T	G	A	G	A	G	C	A	C	T	T	C	T	G	C	T	A	A	C	A	T	1040
GRVER5.SEQ	G	C	T	G	C	G	G	T	T	T	T	G	G	T	T	T	G	A	C	T	G	A	G	A	G	C	A	C	T	T	C	T	G	C	T	A	A	C	A	T	1040
GRVER4.SEQ	G	C	T	G	C	G	G	T	T	T	T	G	G	T	T	T	G	A	C	T	G	A	G	A	G	C	A	C	T	T	C	T	G	C	T	A	A	C	A	T	1040
GRVER3.SEQ	G	C	T	G	C	G	G	T	T	T	T	G	G	T	T	T	G	A	C	T	G	A	G	A	G	C	A	C	T	T	C	T	G	C	C	A	A	C	A	T	1040
GRVER2.SEQ	G	C	T	G	C	G	G	C	T	T	T	G	G	T	C	T	G	A	C	T	G	A	G	A	G	C	A	C	C	T	C	T	G	C	T	A	A	C	A	T	1040
GRVER1.SEQ	G	C	T	G	C	G	G	C	T	T	T	G	G	T	C	T	G	A	C	T	G	A	G	A	G	C	A	C	C	T	C	T	G	C	T	A	A	C	A	T	1040
YG81-6G1.SEQ	G	C	T	G	T	G	G	A	T	T	T	G	G	T	T	T	G	A	C	A	G	A	A	T	C	T	A	C	T	T	C	A	G	C	T	A	A	T	A	T	1040
RDVER1.SEQ	G	T	T	G	T	G	G	T	T	T	C	G	G	C	T	T	G	A	C	C	G	A	A	T	C	T	A	C	T	A	G	C	G	C	C	A	T	T	A	T	1040
RDVER2.SEQ	G	T	T	G	T	G	G	T	T	T	C	G	G	C	T	T	G	A	C	C	G	A	A	T	C	T	A	C	T	A	G	C	G	C	C	A	T	T	A	T	1040
RDVER3.SEQ	G	T	T	G	T	G	G	C	T	T	C	G	G	C	C	T	C	A	C	C	G	A	A	T	C	T	A	C	C	A	G	C	G	C	T	A	T	T	A	T	1040
RDVER4.SEQ	G	T	T	G	T	G	G	C	T	T	C	G	G	C	C	T	C	A	C	C	G	A	A	T	C	T	A	C	C	A	G	C	G	C	T	A	T	T	A	T	1040
RDVER5.SEQ	G	T	T	G	T	G	G	C	T	T	C	G	G	C	C	T	C	A	C	C	G	A	A	T	C	T	A	C	C	A	G	C	G	C	T	A	T	T	A	T	1040
RD7.SEQ	G	T	T	G	T	G	G	C	T	T	C	G	G	C	C	T	C	A	C	C	G	A	A	T	C	T	A	C	C	A	G	C	G	C	T	A	T	T	A	T	1040
RDVER51.SEQ	G	T	T	G	T	G	G	C	T	T	C	G	G	C	C	T	C	A	C	C	G	A	A	T	C	T	A	C	C	A	G	C	G	C	T	A	T	T	A	T	1040
RDVER52.SEQ	G	T	T	G	T	G	G	C	T	T	C	G	G	C	C	T	C	A	C	C	G	A	A	T	C	T	A	C	C	A	G	C	G	C	T	A	T	T	A	T	1040
RD1561H9.SEQ	G	T	T	G	T	G	G	C	T	T	C	G	G	C	C	T	C	A	C	C	G	A	A	T	C	T	A	C	C	A	G	T	G	C	G	A	T	T	A	T	1040

GRVER51.SEQ	C	C	A	T	A	G	C	T	T	G	C	G	A	G	A	C	G	A	G	T	T	T	A	A	G	T	C	T	G	G	T	A	G	C	C	T	G	G	G	T	1080	
GR6.SEQ	C	C	A	T	A	G	C	T	T	G	C	G	A	G	A	C	G	A	G	T	T	T	A	A	G	T	C	T	G	G	T	A	G	C	C	T	G	G	G	T	1080	
GRVER5.SEQ	C	C	A	T	A	G	C	T	T	G	C	G	A	G	A	C	G	A	G	T	T	T	A	A	G	T	C	T	G	G	T	A	G	C	C	T	G	G	G	T	1080	
GRVER4.SEQ	C	C	A	T	A	G	C	T	T	G	C	G	A	G	A	C	G	A	G	T	T	T	A	A	G	T	C	T	G	G	T	A	G	C	C	T	G	G	G	T	1080	
GRVER3.SEQ	C	C	A	T	A	G	C	T	T	G	C	G	T	G	A	C	G	A	G	T	T	T	A	A	A	T	C	T	G	G	T	A	G	C	C	T	G	G	G	T	1080	
GRVER2.SEQ	T	C	A	T	A	G	C	T	T	G	C	G	T	G	A	T	G	A	G	T	T	C	A	A	A	T	C	T	G	G	C	A	G	C	C	T	G	G	G	T	1080	
GRVER1.SEQ	T	C	A	T	A	G	C	T	T	G	C	G	T	G	A	T	G	A	A	T	T	C	A	A	A	T	C	T	G	G	C	A	G	C	C	T	G	G	G	T	1080	
YG81-6G1.SEQ	A	C	A	C	A	G	T	C	T	T	A	G	G	G	A	T	G	A	A	T	T	T	A	A	A	T	C	A	G	G	A	T	C	A	C	T	T	G	G	A	1080	
RDVER1.SEQ	C	C	A	A	T	C	T	C	T	T	G	C	G	C	G	A	C	G	A	G	T	T	T	A	A	G	A	G	C	G	G	T	T	C	T	T	T	G	G	G	C	1080
RDVER2.SEQ	C	C	A	A	T	C	T	C	T	T	G	C	G	C	G	A	C	G	A	A	T	T	T	A	A	G	A	G	C	G	G	T	T	C	T	T	T	G	G	G	C	1080
RDVER3.SEQ	T	C	A	A	T	C	T	C	T	C	C	G	C	G	A	T	G	A	G	T	T	T	A	A	G	A	G	C	G	G	C	T	C	T	T	T	G	G	G	C	1080	
RDVER4.SEQ	T	C	A	G	T	C	T	C	T	C	C	G	C	G	A	T	G	A	G	T	T	T	A	A	G	A	G	C	G	G	C	T	C	T	T	T	G	G	G	C	1080	
RDVER5.SEQ	T	C	A	G	T	C	T	C	T	C	C	G	C	G	A	T	G	A	G	T	T	T	A	A	G	A	G	C	G	G	C	T	C	T	T	T	G	G	G	C	1080	
RD7.SEQ	T	C	A	G	T	C	T	C	T	C	C	G	C	G	A	T	G	A	G	T	T	T	A	A	G	A	G	C	G	G	C	T	C	T	T	T	G	G	G	C	1080	
RDVER51.SEQ	T	C	A	G	T	C	T	C	T	C	C	G	C	G	A	T	G	A	G	T	T	T	A	A	G	A	G	C	G	G	C	T	C	T	T	T	G	G	G	C	1080	
RDVER52.SEQ	T	C	A	G	T	C	T	C	T	C	G	G	G	A	T	G	A	G	T	T	T	A	A	G	A	G	C	G	G	C	T	C	T	T	T	G	G	G	C	1080		
RD1561H9.SEQ	C	C	A	G	A	C	T	C	T	C	G	G	G	A	T	G	A	G	T	T	T	A	A	G	A	G	C	G	G	C	T	C	T	T	T	G	G	G	C	1080		

Figure 2 (Cont.)

GRVER51.SEQ	C	G	C	G	T	G	A	C	T	C	T	T	A	T	G	G	C	T	G	C	A	A	A	G	A	T	C	G	C	G	A	C	C	G	T	G	1120					
GR6.SEQ	C	G	C	G	T	G	A	C	T	C	T	T	A	T	G	G	C	T	G	C	A	A	A	G	A	T	C	G	C	G	A	C	C	G	T	G	1120					
GRVER5.SEQ	C	G	C	G	T	G	A	C	T	C	T	T	A	T	G	G	C	T	G	C	A	A	A	G	A	T	C	G	C	G	A	C	C	G	T	G	1120					
GRVER4.SEQ	C	G	C	G	T	G	A	C	T	C	T	C	T	A	T	G	G	C	T	G	C	A	A	A	G	A	T	C	G	C	G	A	C	C	G	T	G	1120				
GRVER3.SEQ	C	G	C	G	T	G	A	C	C	C	T	T	G	A	T	G	G	C	T	G	C	A	A	A	G	A	T	C	G	C	G	A	C	C	G	T	G	1120				
GRVER2.SEQ	C	G	C	G	T	G	A	C	T	C	C	T	T	G	A	T	G	G	C	C	G	C	T	A	A	G	A	T	C	G	C	G	A	C	C	G	T	G	1120			
GRVER1.SEQ	C	G	C	G	T	G	A	C	T	C	C	T	T	G	A	T	G	G	C	C	G	C	T	A	A	G	A	T	C	G	C	G	A	C	C	G	T	G	1120			
YG81-6G1.SEQ	A	G	A	G	T	A	C	T	C	C	T	T	A	A	T	G	G	C	A	G	C	T	A	A	A	A	T	A	G	C	A	G	A	T	A	G	G	G	1120			
RDVER1.SEQ	C	G	T	G	T	C	A	C	C	C	A	C	T	G	A	T	G	G	C	T	G	C	C	A	A	A	A	T	T	G	C	T	G	A	T	C	G	C	G	1120		
RDVER2.SEQ	C	G	T	G	T	C	A	C	C	C	A	C	T	G	A	T	G	G	C	T	G	C	C	A	A	A	A	T	T	G	C	T	G	A	T	C	G	C	G	1120		
RDVER3.SEQ	C	G	T	G	T	C	A	C	T	C	C	A	C	T	C	A	T	G	G	C	T	G	C	T	A	A	A	A	T	C	G	C	T	G	A	T	C	G	C	G	1120	
RDVER4.SEQ	C	G	T	G	T	C	A	C	T	C	C	A	C	T	C	A	T	G	G	C	T	G	C	T	A	A	A	G	A	T	C	G	C	T	G	A	T	C	G	C	G	1120
RDVER5.SEQ	C	G	T	G	T	C	A	C	T	C	C	A	C	T	C	A	T	G	G	C	T	G	C	T	A	A	G	A	T	C	G	C	T	G	A	T	C	G	C	G	1120	
RD7.SEQ	C	G	T	G	T	C	A	C	T	C	C	A	C	T	C	A	T	G	G	C	T	G	C	T	A	A	G	A	T	C	G	C	T	G	A	T	C	G	C	G	1120	
RDVER51.SEQ	C	G	T	G	T	C	A	C	T	C	C	A	C	T	C	A	T	G	G	C	T	G	C	T	A	A	G	A	T	C	G	C	T	G	A	T	C	G	C	G	1120	
RDVER52.SEQ	C	G	T	G	T	C	A	C	T	C	C	A	C	T	C	A	T	G	G	C	T	G	C	T	A	A	G	A	T	C	G	C	T	G	A	T	C	G	C	G	1120	
RD1561H9.SEQ	C	G	T	G	T	C	A	C	T	C	C	A	C	T	C	A	T	G	G	C	T	G	C	T	A	A	G	A	T	C	G	C	T	G	A	T	C	G	C	G	1120	

GRVER51.SEQ	A	G	A	C	G	G	C	A	A	G	C	A	C	T	G	G	G	C	C	A	A	A	T	C	A	A	G	T	C	G	G	T	G	A	A	T	T	1160				
GR6.SEQ	A	G	A	C	G	G	C	A	A	G	C	A	C	T	G	G	G	C	C	A	A	A	T	C	A	A	G	T	C	G	G	T	G	A	A	T	1160					
GRVER5.SEQ	A	G	A	C	G	G	C	A	A	G	C	A	C	T	G	G	G	C	C	A	A	A	T	C	A	A	G	T	C	G	G	T	G	A	A	T	1160					
GRVER4.SEQ	A	G	A	C	G	G	C	A	A	G	C	A	C	T	G	G	G	C	C	A	A	A	T	C	A	A	G	T	C	G	G	T	G	A	A	T	1160					
GRVER3.SEQ	A	G	A	C	G	G	C	A	A	G	C	C	C	T	G	G	G	C	C	A	A	A	T	C	A	G	G	T	C	G	G	T	G	A	A	T	1160					
GRVER2.SEQ	A	G	A	C	G	G	C	A	A	G	C	T	C	T	G	G	G	T	C	C	A	A	A	T	C	A	A	G	T	C	G	G	C	G	A	A	T	1160				
GRVER1.SEQ	A	G	A	C	G	G	C	A	A	G	C	T	C	T	G	G	G	T	C	C	A	A	A	T	C	A	A	G	T	C	G	G	C	G	A	A	T	1160				
YG81-6G1.SEQ	A	A	A	C	T	G	G	T	A	A	G	C	A	T	T	G	G	G	A	C	C	A	A	A	T	C	A	A	G	T	T	G	G	T	G	A	A	T	1160			
RDVER1.SEQ	A	A	A	C	T	G	G	T	A	A	G	G	C	C	T	T	G	G	G	C	C	C	T	A	A	C	C	A	G	G	T	G	G	G	T	G	A	G	C	T	1160	
RDVER2.SEQ	A	A	A	C	T	G	G	T	A	A	G	G	C	C	T	T	G	G	G	C	C	C	T	A	A	C	C	A	G	G	T	G	G	G	T	G	A	G	C	T	1160	
RDVER3.SEQ	A	A	A	C	T	G	G	T	A	A	G	G	C	C	T	T	T	G	G	G	C	C	C	T	A	A	C	C	A	A	G	T	G	G	G	C	G	A	G	C	T	1160
RDVER4.SEQ	A	A	A	C	T	G	G	T	A	A	G	G	C	C	T	T	T	G	G	G	C	C	C	T	A	A	C	C	A	A	G	T	G	G	G	C	G	A	G	C	T	1160
RDVER5.SEQ	A	A	A	C	T	G	G	T	A	A	G	G	C	C	T	T	T	G	G	G	C	C	C	T	A	A	C	C	A	A	G	T	G	G	G	C	G	A	G	C	T	1160
RD7.SEQ	A	A	A	C	T	G	G	T	A	A	G	G	C	C	T	T	T	G	G	G	C	C	C	G	A	A	C	C	A	A	G	T	G	G	G	C	G	A	G	C	T	1160
RDVER51.SEQ	A	A	A	C	T	G	G	T	A	A	G	G	C	C	T	T	T	G	G	G	C	C	C	G	A	A	C	C	A	A	G	T	G	G	G	C	G	A	G	C	T	1160
RDVER52.SEQ	A	A	A	C	T	G	G	T	A	A	G	G	C	C	T	T	T	G	G	G	C	C	C	G	A	A	C	C	A	A	G	T	G	G	G	C	G	A	G	C	T	1160
AD1561H9.SEQ	A	A	A	C	T	G	G	T	A	A	G	G	C	C	T	T	T	G	G	G	C	C	C	G	A	A	C	C	A	A	G	T	G	G	G	C	G	A	G	C	T	1160

GRVER51.SEQ	G	T	G	T	A	T	T	A	A	G	G	G	C	C	T	A	T	G	G	T	C	T	C	T	A	A	A	G	G	C	T	A	C	G	T	G	A	A	C	1200		
GR6.SEQ	G	T	G	T	A	T	T	A	A	G	G	G	C	C	C	T	A	T	G	G	T	C	T	C	T	A	A	A	G	G	C	T	A	C	G	T	G	A	A	C	1200	
GRVER5.SEQ	G	T	G	T	A	T	T	A	A	G	G	G	C	C	C	T	A	T	G	G	T	C	T	C	T	A	A	A	G	G	C	T	A	C	G	T	G	A	A	C	1200	
GRVER4.SEQ	G	T	G	T	A	T	T	A	A	G	G	G	C	C	C	T	A	T	G	G	T	C	T	C	T	A	A	A	G	G	C	T	A	C	G	T	G	A	A	C	1200	
GRVER3.SEQ	G	T	G	C	A	T	T	A	A	G	G	G	C	C	C	T	A	T	G	G	T	C	T	C	T	A	A	A	G	G	C	T	A	C	G	T	G	A	A	C	1200	
GRVER2.SEQ	G	T	G	T	A	T	T	A	A	G	G	G	T	C	C	T	A	T	G	G	T	G	T	C	T	A	A	A	G	G	C	T	A	C	G	T	C	A	A	C	1200	
GRVER1.SEQ	G	T	G	T	A	T	T	A	A	G	G	G	T	C	C	T	A	T	G	G	T	G	T	C	T	A	A	A	G	G	C	T	A	C	G	T	C	A	A	C	1200	
YG81-6G1.SEQ	A	T	G	C	A	T	T	A	A	A	G	G	T	C	C	C	A	T	G	G	T	A	T	C	G	A	A	A	G	G	T	T	A	C	G	T	G	A	A	C	1200	
RDVER1.SEQ	G	T	G	C	A	T	C	A	A	A	G	G	C	C	C	A	A	T	G	G	T	C	A	G	C	A	A	A	G	G	G	T	T	A	T	G	T	G	A	A	T	1200
RDVER2.SEQ	G	T	G	C	A	T	C	A	A	A	G	G	C	C	C	A	A	T	G	G	T	C	A	G	C	A	A	A	G	G	G	T	T	A	T	G	T	G	A	A	T	1200
RDVER3.SEQ	G	T	G	T	A	T	C	A	A	A	G	G	C	C	C	T	A	T	G	G	T	G	A	G	C	A	A	A	G	G	G	T	T	A	T	G	T	C	A	A	T	1200
RDVER4.SEQ	G	T	G	T	A	T	C	A	A	A	G	G	C	C	C	T	A	T	G	G	T	G	A	G	C	A	A	A	G	G	G	T	T	A	T	G	T	C	A	A	T	1200
RDVER5.SEQ	G	T	G	T	A	T	C	A	A	A	G	G	C	C	C	T	A	T	G	G	T	G	A	G	C	A	A	A	G	G	G	T	T	A	T	G	T	C	A	A	T	1200
RD7.SEQ	G	T	G	T	A	T	C	A	A	A	G	G	C	C	C	T	A	T	G	G	T	G	A	G	C	A	A	A	G	G	G	T	T	A	T	G	T	C	A	A	T	1200
RDVER51.SEQ	G	T	G	T	A	T	C	A	A	A	G	G	C	C	C	T	A	T	G	G	T	G	A	G	C	A	A	A	G	G	G	T	T	A	T	G	T	C	A	A	T	1200
RDVER52.SEQ	G	T	G	T	A	T	C	A	A	A	G	G	C	C	C	T	A	T	G	G	T	G	A	G	C	A	A	A	G	G	G	T	T	A	T	G	T	C	A	A	T	1200
RD1561H9.SEQ	G	T	G	T	A	T	C	A	A	A	G	G	C	C	C	T	A	T	G	G	T	G	A	G	C	A	A	A	G	G	G	T	T	A	T	G	T	C	A	A	T	1200



GRVER51.SEQ	T	A	C	A	A	A	G	G	C	T	C	A	A	G	T	C	G	C	A	C	C	A	G	C	C	G	A	A	A	A	1360	
GR6.SEQ	T	A	C	A	A	A	G	G	C	T	C	T	C	A	A	G	T	C	G	C	A	C	C	A	G	C	C	G	A	A	A	1360
GRVER5.SEQ	T	A	C	A	A	A	G	G	C	T	C	T	C	A	A	G	T	C	G	C	A	C	C	A	G	C	C	G	A	A	A	1360
GRVER4.SEQ	T	A	C	A	A	A	G	G	C	T	C	T	C	A	A	G	T	C	G	C	C	C	A	G	C	C	G	A	A	A	A	1360
GRVER3.SEQ	T	A	C	A	A	A	G	G	C	T	C	T	C	A	A	G	T	C	G	C	C	C	A	G	C	T	G	A	A	A	A	1360
GRVER2.SEQ	T	A	T	A	A	A	G	G	C	T	C	T	C	A	A	G	T	C	G	C	C	C	A	G	C	T	G	A	G	A	A	1360
GRVER1.SEQ	T	A	T	A	A	A	G	G	C	T	C	T	C	A	G	G	T	C	G	C	C	C	A	G	C	T	G	A	G	A	A	1360
YG81-6G1.SEQ	T	A	T	A	A	G	G	G	C	T	C	T	C	A	G	G	T	A	G	C	A	C	C	T	G	C	A	G	A	A	A	1360
RDVER1.SEQ	T	A	C	A	A	G	G	G	T	A	G	C	C	A	A	G	T	G	G	C	T	C	C	T	G	C	C	G	A	A	A	1360
RDVER2.SEQ	T	A	C	A	A	G	G	G	T	A	G	C	C	A	A	G	T	G	G	C	T	C	C	T	G	C	C	G	A	A	A	1360
RDVER3.SEQ	T	A	C	A	A	G	G	G	T	A	G	C	C	A	G	G	T	G	G	C	T	C	C	A	G	C	C	G	A	A	A	1360
RDVER4.SEQ	T	A	C	A	A	G	G	G	T	A	G	C	C	A	G	G	T	T	G	C	T	C	C	A	G	C	T	G	A	A	A	1360
RDVER5.SEQ	T	A	C	A	A	G	G	G	T	A	G	C	C	A	G	G	T	T	G	C	T	C	C	A	G	C	T	G	A	A	A	1360
RD7.SEQ	T	A	C	A	A	G	G	G	T	A	G	C	C	A	G	G	T	T	G	C	T	C	C	A	G	C	T	G	A	A	A	1360
RDVER51.SEQ	T	A	C	A	A	G	G	G	T	A	G	C	C	A	G	G	T	T	G	C	T	C	C	A	G	C	T	G	A	A	A	1360
RDVER52.SEQ	T	A	C	A	A	G	G	G	T	A	G	C	C	A	G	G	T	T	G	C	T	C	C	A	G	C	T	G	A	A	A	1360
RD1561H9.SEQ	T	A	C	A	A	G	G	G	T	A	G	C	C	A	G	G	T	T	G	C	T	C	C	A	G	C	T	G	A	A	A	1360

GRVER51.SEQ	T	T	T	T	G	C	T	G	A	A	G	A	A	C	C	C	T	T	G	T	A	T	C	C	G	C	G	A	C	G	T	G	G	C	C	G	T	C	G	T	1400
GR6.SEQ	T	T	T	T	G	C	T	G	A	A	G	A	A	C	C	C	T	T	G	T	A	T	C	C	G	C	G	A	C	G	T	G	G	C	C	G	T	C	G	T	1400
GRVER5.SEQ	T	T	T	T	G	C	T	G	A	A	G	A	A	C	C	C	T	T	G	T	A	T	C	C	G	C	G	A	C	G	T	G	G	C	C	G	T	C	G	T	1400
GRVER4.SEQ	T	T	T	T	G	C	T	G	A	A	G	A	A	C	C	C	T	T	G	T	A	T	C	C	G	C	G	A	C	G	T	G	G	C	C	G	T	C	G	T	1400
GRVER3.SEQ	T	T	T	T	G	C	T	G	A	A	G	A	A	C	C	C	T	T	G	T	A	T	T	C	G	C	G	A	C	G	T	G	G	C	C	G	T	C	G	T	1400
GRVER2.SEQ	T	C	T	T	G	C	T	G	A	A	G	A	A	C	C	C	T	T	G	C	A	T	T	C	G	T	G	A	C	G	T	G	G	C	C	G	T	C	G	T	1400
GRVER1.SEQ	T	C	T	T	G	C	T	G	A	A	G	A	A	C	C	C	T	T	G	C	A	T	T	C	G	T	G	A	C	G	T	G	G	C	C	G	T	C	G	T	1400
YG81-6G1.SEQ	T	T	T	T	A	T	T	G	A	A	A	A	A	T	C	C	A	T	G	T	A	T	C	A	G	A	G	A	T	G	T	T	G	C	T	G	T	G	G	T	1400
RDVER1.SEQ	T	T	C	T	G	T	T	G	A	A	A	A	A	T	C	C	A	T	G	T	A	T	C	C	G	C	G	A	T	G	T	C	G	C	T	G	T	G	G	T	1400
RDVER2.SEQ	T	T	C	T	G	T	T	G	A	A	A	A	A	T	C	C	A	T	G	T	A	T	C	C	G	C	G	A	T	G	T	C	G	C	T	G	T	G	G	T	1400
RDVER3.SEQ	T	T	C	T	G	T	T	G	A	A	A	A	A	T	C	C	A	T	G	C	A	T	C	C	G	T	G	A	T	G	T	C	G	C	T	G	T	G	G	T	1400
RDVER4.SEQ	T	T	C	T	G	T	T	G	A	A	A	A	A	T	C	C	A	T	G	C	A	T	T	C	G	C	G	A	T	G	T	C	G	C	T	G	T	G	G	T	1400
RDVER5.SEQ	T	T	C	T	G	T	T	G	A	A	A	A	A	T	C	C	A	T	G	C	A	T	T	C	G	C	G	A	T	G	T	C	G	C	T	G	T	G	G	T	1400
=RD7.SEQ	T	T	C	T	G	T	T	G	A	A	A	A	A	T	C	C	A	T	G	C	A	T	T	C	G	C	G	A	T	G	T	C	G	C	T	G	T	G	G	T	1400
RDVER51.SEQ	T	T	C	T	G	T	T	G	A	A	A	A	A	T	C	C	A	T	G	C	A	T	T	C	G	C	G	A	T	G	T	C	G	C	T	G	T	G	G	T	1400
RDVER52.SEQ	T	T	C	T	G	T	T	G	A	A	A	A	A	T	C	C	A	T	G	C	A	T	T	C	G	C	G	A	T	G	T	C	G	C	T	G	T	G	G	T	1400
RD1561H9.SEQ	T	T	C	T	G	T	T	G	A	A	A	A	A	T	C	C	A	T	G	C	A	T	T	C	G	C	G	A	T	G	T	C	G	C	T	G	T	G	G	T	1400

GRVER51.SEQ	G	G	G	T	A	T	C	C	C	A	G	A	C	T	T	G	G	A	A	G	C	T	G	G	C	G	A	G	T	T	G	C	C	T	A	G	C	G	C	C	1440
GR6.SEQ	G	G	G	T	A	T	C	C	C	A	G	A	C	T	T	G	G	A	A	G	C	T	G	G	C	G	A	G	T	T	G	C	C	T	A	G	C	G	C	C	1440
GRVER5.SEQ	G	G	G	T	A	T	C	C	C	A	G	A	C	T	T	G	G	A	A	G	C	T	G	G	C	G	A	G	T	T	G	C	C	T	A	G	C	G	C	C	1440
GRVER4.SEQ	G	G	G	T	A	T	C	C	C	A	G	A	C	T	T	G	G	A	A	G	C	T	G	G	T	G	A	G	T	T	G	C	C	T	A	G	C	G	C	C	1440
GRVER3.SEQ	G	G	G	T	A	T	C	C	C	A	G	A	C	T	T	G	G	A	A	G	C	T	G	G	C	G	A	G	T	T	G	C	C	T	A	G	C	G	C	C	1440
GRVER2.SEQ	G	G	G	T	A	T	C	C	C	A	G	A	T	T	T	G	G	A	A	G	C	T	G	G	C	G	A	G	C	T	G	C	C	T	A	G	C	G	C	C	1440
GRVER1.SEQ	G	G	G	T	A	T	C	C	C	A	G	A	T	T	T	G	G	A	A	G	C	T	G	G	C	G	A	G	C	T	G	C	C	T	A	G	C	G	C	C	1440
YG81-6G1.SEQ	T	G	G	T	A	T	T	C	C	T	G	A	T	C	T	A	G	A	A	G	C	T	G	G	A	G	A	A	C	T	G	C	C	A	T	C	T	G	C	G	1440
RDVER1.SEQ	C	G	G	C	A	T	T	C	C	T	G	A	C	C	T	G	G	A	G	G	C	C	G	G	T	G	A	A	T	T	G	C	C	A	T	C	T	G	C	T	1440
RDVER2.SEQ	C	G	G	C	A	T	T	C	C	T	G	A	C	C	T	G	G	A	G	G	C	C	G	G	T	G	A	A	T	T	G	C	C	A	T	C	T	G	C	T	1440
RDVER3.SEQ	C	G	G	C	A	T	T	C	C	T	G	A	T	C	T	G	G	A	G	G	C	C	G	G	T	G	A	A	C	T	G	C	C	T	T	C	T	G	C	T	1440
RDVER4.SEQ	C	G	G	C	A	T	T	C	C	T	G	A	T	C	T	G	G	A	G	G	C	C	G	G	C	G	A	A	C	T	G	C	C	T	T	C	T	G	C	T	1440
RDVER5.SEQ	C	G	G	C	A	T	T	C	C	T	G	A	T	C	T	G	G	A	G	G	C	C	G	G	C	G	A	A	C	T	G	C	C	T	T	C	T	G	C	T	1440
RD7.SEQ	C	G	G	C	A	T	T	C	C	T	G	A	T	C	T	G	G	A	G	G	C	C	G	G	C	G	A	A	C	T	G	C	C	T	T	C	T	G	C	T	1440
RDVER51.SEQ	C	G	G	C	A	T	T	C	C	T	G	A	T	C	T	G	G	A	G	G	C	C	G	G	C	G	A	A	C	T	G	C	C	T	T	C	T	G	C	T	1440
RDVER52.SEQ	C	G	G	C	A	T	T	C	C	T	G	A	T	C	T	G	G	A	G	G	C	C	G	G	C	G	A	A	C	T	G	C	C	T	T	C	T	G	C	T	1440
RD1561H9.SEQ	C	G	G	C	A	T	T	C	C	T	G	A	T	C	T	G	G	A	G	G	C	C	G	G	C	G	A	A	C	T	G	C	C	T	T	C	T	G	C	T	1440

Figure 2 (cont.)

GRVER51.SEQ T T T G T G G T G A A C A A A C C C G G C A A G G A G A T C A C T G C T A A G G 1480
 GR6.SEQ T T T G T G G T G A A A C A A C C C G G C A A G G A G A T C A C T G C T A A G G 1480
 GRVER5.SEQ T T T G T G G T G A A A C A A C C C G G C A A G G A G A T C A C T G C T A A G G 1480
 GRVER4.SEQ T T T G T G G T G A A A C A A C C T G G A A A G G A G A T C A C T G C T A A G G 1480
 GRVER3.SEQ T T T G T G G T G A A A C A A C C T G G C A A G G A G A T T A C T G C T A A G G 1480
 GRVER2.SEQ T T T G T C G T G A A A C A A C C A G G C A A G G A A A T T A C C G C T A A A G 1480
 GRVER1.SEQ T T T G T C G T G A A A C A A C C A G G T A A G G A A A T T A C C G C T A A A G 1480
 YG81-6G1.SEQ T T T G T G G T T A A A C A G C C C G G A A A G G A G A T T A C A G C T A A A G 1480
 RDVER1.SEQ T T C G T G G T C A A G C A G C C T G G C A A A G A G A T C A C T G C C A A G G 1480
 RDVER2.SEQ T T C G T G G T C A A G C A G C C T G G T A A A G A G A T C A C T G C C A A G G 1480
 RDVER3.SEQ T T C G T C G T C A A G C A G C C T G G T A A A G A A A T C A C C G C C A A A G 1480
 RDVER4.SEQ T T C G T T G T C A A G C A G C C T G G T A A A G A A A T T A C C G C C A A A G 1480
 RDVER5.SEQ T T C G T T G T C A A G C A G C C T G G T A A A G A A A T T A C C G C C A A A G 1480
 RD7.SEQ T T C G T T G T C A A G C A G C C T G G T A A A G A A A T T A C C G C C A A A G 1480
 RDVER51.SEQ T T C G T T G T C A A G C A G C C T G G T A A A G A A A T T A C C G C C A A A G 1480
 RDVER52.SEQ T T C G T T G T C A A G C A G C C T G G T A A A G A A A T T A C C G C C A A A G 1480
 RD1561H9.SEQ T T C G T T G T C A A G C A G C C T G G T A C A G A A A T T A C C G C C A A A G 1480

GRVER51.SEQ A G G T C T A C G A C T A T T T G G C C G A G C G C G T G T C T C A C A C C A A 1520
 GR6.SEQ A G G T C T A C G A C T A T T T G G C C G A G C G C G T G T C T C A C A C C A A 1520
 GRVER5.SEQ A G G T C T A C G A C T A T T T G G C C G A G C G C G T G T C T C A C A C C A A 1520
 GRVER4.SEQ A G G T C T A C G A C T A T T T G G C C G A G C G C G T G T C T C A C A C C A A 1520
 GRVER3.SEQ A G G T C T A C G A C T A T T T G G C C G A G C G C G T G T C T C A C A C T A A 1520
 GRVER2.SEQ A G G T C T A C G A C T A T T T G G C C G A G C G C G T G T C T C A C A C T A A 1520
 GRVER1.SEQ A G G T C T A C G A C T A T T T G G C C G A A C G C G T G T C T C A C A C T A A 1520
 YG81-6G1.SEQ A A G T G T A C G A T T A T C T T G C C G A G A G G G T C T C C A T A C A A A 1520
 RDVER1.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G T C A G C C A T A C C A A 1520
 RDVER2.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G T C A G C C A T A C C A A 1520
 RDVER3.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C C A A 1520
 RDVER4.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A 1520
 RDVER5.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A 1520
 RD7.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A 1520
 RDVER51.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A 1520
 RDVER52.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A 1520
 RD1561H9.SEQ A A G T G T A T G A T T A C C T G G C T G A A C G T G T G A G C C A T A C T A A 1520

GRVER51.SEQ A T A T C T G C G T G G C G G C G T C C G C T T C G T C G A T T C T A T T C C A 1560
 GR6.SEQ A T A T C T G C G T G G C G G C G T C C G C T T C G T C G A T T C T A T T C C A 1560
 GRVER5.SEQ A T A T C T G C G T G G C G G C G T C C G C T T C G T C G A T T C T A T T C C A 1560
 GRVER4.SEQ A T A T C T G C G T G G C G G C G T C C G C T T C G T C G A T T C C A T C C C A 1560
 GRVER3.SEQ A T A T C T G C G T G G C G G C G T C C G C T T C G T C G A T T C T A T C C C T 1560
 GRVER2.SEQ G T A C C T G C G T G G C G G T G T C C G C T T C G T C G A T A G C A T C C C T 1560
 GRVER1.SEQ G T A C C T G C G T G G C G G T G T C C G C T T C G T G G A T A G C A T C C C T 1560
 YG81-6G1.SEQ G T A T T T G C G T G G A G G G T T C G A T T C G T T G A T A G C A T A C C A 1560
 RDVER1.SEQ A T A T T T G C G C G G T G G C G T G C G T T T T G T G G A C T C T A T T C C A 1560
 RDVER2.SEQ A T A T T T G C G C G G T G G C G T G C G T T T T G T G G A C T C T A T T C C A 1560
 RDVER3.SEQ G T A C T T G C G T G G C G G C G T G C G T T T T G T G G A C A G C A T T C C A 1560
 RDVER4.SEQ G T A C T T G C G T G G C G G C G T G C G T T T T G T G G A T A G C A T T C C T 1560
 RDVER5.SEQ G T A C T T G C G T G G C G G C G T G C G T T T T G T T G A C T C C A T C C C T 1560
 RD7.SEQ G T A C T T G C G T G G C G G C G T G C G T T T T G T T G A C T C C A T C C C T 1560
 RDVER51.SEQ G T A C T T G C G T G G C G G C G T G C G T T T T G T T G A C T C C A T C C C T 1560
 RDVER52.SEQ G T A C T T G C G T G G C G G C G T G C G T T T T G T T G A C T C C A T C C C T 1560
 RD1561H9.SEQ G T A C T T G C G T G G C G G C G T G C G T T T T G T T G A C T C C A T C C C T 1560

Figure 2 (cont.)

GRVER51.SEQ	C	G	C	A	A	C	G	T	T	A	C	C	G	G	T	A	A	G	A	T	C	A	C	T	C	G	T	A	A	A	G	A	G	T	T	G	C	T	G	A	1600
GR6.SEQ	C	G	C	A	A	C	G	T	T	A	C	C	G	G	T	A	A	G	A	T	C	A	C	T	C	G	T	A	A	A	G	A	G	T	T	G	C	T	G	A	1600
GRVER5.SEQ	C	G	C	A	A	C	G	T	T	A	C	C	G	G	T	A	A	G	A	T	C	A	C	T	C	G	T	A	A	A	G	A	G	T	T	G	C	T	G	A	1600
GRVER4.SEQ	C	G	C	A	A	C	G	T	G	A	C	C	G	G	T	A	A	G	A	T	C	A	C	T	C	G	T	A	A	A	G	A	A	T	T	G	C	T	G	A	1600
GRVER3.SEQ	C	G	C	A	A	C	G	T	C	A	C	C	G	G	C	A	A	G	A	T	C	A	C	T	C	G	T	A	A	A	G	A	G	T	T	G	C	T	G	A	1600
GRVER2.SEQ	C	G	C	A	A	T	G	T	C	A	C	C	G	G	C	A	A	A	A	T	T	A	C	T	C	G	T	A	A	G	G	A	G	T	T	G	C	T	G	A	1600
GRVER1.SEQ	C	G	C	A	A	T	G	T	C	A	C	C	G	G	C	A	A	A	A	T	T	A	C	T	C	G	T	A	A	G	G	A	G	T	T	G	C	T	G	A	1600
YG81-6G1.SEQ	A	G	G	A	A	T	G	T	T	A	C	A	G	G	T	A	A	A	A	T	T	A	C	A	A	G	A	A	A	G	G	A	A	C	T	T	C	T	G	A	1600
RDVER1.SEQ	C	G	T	A	A	C	G	T	G	A	C	T	G	G	T	A	A	G	A	T	C	A	C	C	C	G	C	A	A	A	G	A	A	C	T	G	T	T	G	A	1600
RDVER2.SEQ	C	G	T	A	A	C	G	T	G	A	C	T	G	G	T	A	A	G	A	T	C	A	C	C	C	G	C	A	A	A	G	A	A	C	T	G	T	T	G	A	1600
RDVER3.SEQ	C	G	T	A	A	T	G	T	G	A	C	T	G	G	T	A	A	A	A	T	T	A	C	C	C	G	C	A	A	G	G	A	A	C	T	G	T	T	G	A	1600
RDVER4.SEQ	C	G	C	A	A	T	G	T	G	A	C	T	G	G	C	A	A	A	A	T	T	A	C	C	C	G	C	A	A	G	G	A	G	C	T	G	T	T	G	A	1600
RDVER5.SEQ	C	G	T	A	A	C	G	T	A	A	C	A	G	G	C	A	A	A	A	T	T	A	C	C	C	G	C	A	A	G	G	A	G	C	T	G	T	T	G	A	1600
RD7.SEQ	C	G	T	A	A	C	G	T	A	A	C	A	G	G	C	A	A	A	A	T	T	A	C	C	C	G	C	A	A	G	G	A	G	C	T	G	T	T	G	A	1600
RDVER51.SEQ	C	G	T	A	A	C	G	T	A	A	C	A	G	G	C	A	A	A	A	T	T	A	C	C	C	G	C	A	A	G	G	A	G	C	T	G	T	T	G	A	1600
RDVER52.SEQ	C	G	T	A	A	C	G	T	A	A	C	A	G	G	C	A	A	A	A	T	T	A	C	C	C	G	C	A	A	G	G	A	G	C	T	G	T	T	G	A	1600
RD1561H9.SEQ	C	G	T	A	A	C	G	T	A	A	C	A	G	G	C	A	A	A	A	T	T	A	C	C	C	G	C	A	A	G	G	A	G	C	T	G	T	T	G	A	1600

GRVER51.SEQ	A	G	C	A	A	C	T	C	C	T	C	G	A	A	A	A	G	C	T	G	G	C	G	G	C	1626		
GR6.SEQ	A	G	C	A	A	C	T	C	C	T	C	G	A	A	A	A	A	G	C	T	G	G	C	G	G	C	1626	
GRVER5.SEQ	A	G	C	A	A	C	T	C	C	T	C	G	A	A	A	A	A	G	C	T	G	G	C	G	G	C	1626	
GRVER4.SEQ	A	G	C	A	A	C	T	C	C	T	C	G	A	A	A	A	A	G	C	T	G	G	C	G	G	C	1626	
GRVER3.SEQ	A	A	C	A	A	T	T	G	C	T	C	G	A	A	A	A	A	G	C	T	G	G	C	G	G	C	1626	
GRVER2.SEQ	A	A	C	A	G	T	T	G	C	T	G	G	A	A	A	A	G	G	C	T	G	G	T	G	G	C	1626	
GRVER1.SEQ	A	A	C	A	G	T	T	G	C	T	G	G	A	A	A	A	G	G	C	T	G	G	T	G	G	C	1626	
YG81-6G1.SEQ	A	G	C	A	G	T	T	G	C	T	G	G	A	G	A	A	G	G	C	G	G	G	A	G	G	T	1626	
RDVER1.SEQ	A	G	C	A	A	C	T	G	T	T	G	G	A	G	A	A	A	G	C	C	G	G	C	G	G	T	1626	
RDVER2.SEQ	A	G	C	A	A	C	T	G	T	T	G	G	A	G	A	A	A	G	C	C	G	G	C	G	G	T	1626	
RDVER3.SEQ	A	G	C	A	A	T	T	G	T	T	G	G	A	G	A	A	A	G	G	C	C	G	G	C	G	G	T	1626
RDVER4.SEQ	A	A	C	A	A	T	T	G	T	T	G	G	A	G	A	A	A	G	G	C	C	G	G	C	G	G	T	1626
RDVER5.SEQ	A	A	C	A	A	T	T	G	T	T	G	G	A	G	A	A	A	G	G	C	C	G	G	C	G	G	T	1626
RD7.SEQ	A	A	C	A	A	T	T	G	T	T	G	G	A	G	A	A	A	G	G	C	C	G	G	C	G	G	T	1626
RDVER51.SEQ	A	A	C	A	A	T	T	G	T	T	G	G	A	G	A	A	A	G	G	C	C	G	G	C	G	G	T	1626
RDVER52.SEQ	A	A	C	A	A	T	T	G	T	T	G	G	A	G	A	A	A	G	G	C	C	G	G	C	G	G	T	1626
RD1561H9.SEQ	A	A	C	A	A	T	T	G	T	T	G	G	T	G	A	A	A	G	G	C	C	G	G	C	G	G	T	1626

Figure 3

GRVER51.SEQ MMKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS SHLPQA 118
 GR6.SEQ MMKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS SHLPQA 118
 GRVER5.SEQ MMKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS SHLPQA 118
 GRVER4.SEQ MMKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS SHLPQA 118
 GRVER3.SEQ MMKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS SHLPQA 118
 GRVER2.SEQ MMKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS SHLPQA 118
 GRVER1.SEQ MMKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS SHLPQA 118
 YG81-6G1.SEQ MMKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS SHLPQA 118
 RDVER1.SEQ MMKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS SHLPQA 118
 RDVER2.SEQ MMKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS SHLPQA 118
 RDVER3.SEQ MMKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS SHLPQA 118
 RDVER4.SEQ MMKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS SHLPQA 118
 RDVER5.SEQ MMKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS SHLPQA 118
 RD7.SEQ MMKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS YLPQA 118
 RDVER51.SEQ MMKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS SHLPQA 118
 RDVER52.SEQ MMKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS SHLPQA 118
 RD1561H9.SEQ MIKREKNV IYGPEPLHPLEDLTAGEMLFRA LRKHS SHLPQA 118

GRVER51.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238
 GR6.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238
 GRVER5.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238
 GRVER4.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238
 GRVER3.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238
 GRVER2.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238
 GRVER1.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238
 YG81-6G1.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238
 RDVER1.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238
 RDVER2.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238
 RDVER3.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238
 RDVER4.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238
 RDVER5.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238
 RD7.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238
 RDVER51.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238
 RDVER52.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238
 RD1561H9.SEQ LVDVVGDESLSYKEFFFEATVLLAQSLHNCGYKMN DVVSI C 238

GRVER51.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358
 GR6.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358
 GRVER5.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358
 GRVER4.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358
 GRVER3.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358
 GRVER2.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358
 GRVER1.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358
 YG81-6G1.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358
 RDVER1.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358
 RDVER2.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358
 RDVER3.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358
 RDVER4.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358
 RDVER5.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358
 RD7.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358
 RDVER51.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358
 RDVER52.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358
 RD1561H9.SEQ AENNTRFFIPVIAAWYIGMIVAPVNESYIPDELCKVMG I S 358

004230.006706.006450

Figure 3 (cont.)

GRVER51.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
 GR6.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
 GRVER5.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
 GRVER4.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
 GRVER3.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
 GRVER2.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
 GRVER1.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
 YG81-6G1.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
 RDVER1.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
 RDVER2.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
 RDVER3.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
 RDVER4.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
 RDVER5.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
 RD7.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
 RDVER51.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
 RDVER52.SEQ F V V K Q P G K E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558
 RD1561H9.SEQ F V V K Q P G T E I T A K E V Y D Y L A E R V S H T K Y L R G G V R F V D S I P 1558

GRVER51.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
 GR6.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
 GRVER5.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
 GRVER4.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
 GRVER3.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
 GRVER2.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
 GRVER1.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
 YG81-6G1.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
 RDVER1.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
 RDVER2.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
 RDVER3.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
 RDVER4.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
 RDVER5.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
 RD7.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
 RDVER51.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
 RDVER52.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
 RD1561H9.SEQ R N V T G K I T R K E L L K Q L L V K A G G 1624

Figure 4 Codon Usage Analysis

per 542 total codons

	YG#81-6G	ver1 GR	ver1 RD	ver5 GR	ver5 RD	HUM
CGA	7	0	0	2	0	3
CGC	1	13	13	11	12	6
CGG	0	0	0	0	0	6
CGT	5	13	13	13	14	3
AGA	6	0	0	0	0	5
Arg AGG	7	0	0	0	0	6
CTA	5	0	0	0	0	3
CTC	4	0	1	12	11	11
CTG	4	28	27	19	18	23
CTT	12	0	0	1	1	6
TTA	17	0	0	0	0	3
Leu TTG	13	27	27	23	25	6
TCA	6	0	0	1	2	5
TCC	2	0	0	4	2	10
TCG	7	0	0	0	0	2
TCT	7	16	15	11	12	7
AGC	2	15	15	14	12	10
Ser AGT	7	0	0	1	2	5
ACA	10	0	0	0	1	8
ACC	2	11	11	8	11	12
ACG	2	0	0	0	0	4
Thr ACT	8	11	11	14	10	7
CCA	9	14	14	9	12	8
CCC	8	0	0	2	1	11
CCG	2	0	0	0	0	4
Pro CCT	9	14	14	17	15	8
GCA	14	0	0	5	4	8
GCC	4	19	18	14	12	16
GCG	5	0	0	0	0	4
Ala GCT	15	18	19	18	21	11
GGA	18	0	0	1	3	9
GGC	3	20	19	21	21	14
GGG	2	0	0	1	1	9
Gly GGT	16	19	20	16	14	6
GTA	13	0	0	1	1	3
GTC	4	25	24	21	26	9
GTG	12	25	25	25	17	17
Val GTT	20	0	0	3	5	6
AAA	23	17	18	19	13	12
Lys AAG	12	18	17	16	22	19
AAC	6	11	11	13	12	12
Asn AAT	16	11	10	9	9	9
CAA	8	7	8	11	7	6
Gln CAG	6	7	7	3	8	18
CAC	6	7	6	7	4	8
His CAT	7	6	7	6	9	5
GAA	26	19	19	19	18	15
Glu GAG	12	19	19	19	20	22
GAC	6	13	13	14	12	16
Asp GAT	20	13	13	12	14	12
TAC	8	10	10	12	13	10
Tyr TAT	11	9	10	7	7	7
TGC	3	6	5	3	4	8
Cys TGT	8	5	6	8	7	5
TTC	11	13	12	15	12	12
Phe TTT	14	12	13	10	13	9
ATA	12	0	0	0	0	3
ATC	7	19	19	23	20	13
Ile ATT	19	19	20	15	19	8
Met ATG	11	11	11	11	11	12
Trp TGG	2	2	2	2	2	7

relative codon usage for each aa (*100)

	YG#81-6G	ver5 GR	ver5 RD	HUM
CGA	27	8	0	10
CGC	4	42	46	21
CGG	0	0	0	19
CGT	19	50	54	9
AGA	23	0	0	19
Arg AGG	27	0	0	21
CTA	9	0	0	6
CTC	7	22	20	21
CTG	7	35	33	44
CTT	22	2	2	11
TTA	31	0	0	6
Leu TTG	24	42	45	11
TCA	19	3	7	13
TCC	6	13	7	25
TCG	23	0	0	6
TCT	23	35	40	18
AGC	6	45	40	26
Ser AGT	23	3	7	13
ACA	45	0	5	25
ACC	9	36	50	40
ACG	9	0	0	12
Thr ACT	36	64	45	22
CCA	32	32	43	26
CCC	29	7	4	35
CCG	7	0	0	12
Pro CCT	32	61	54	27
GCA	37	13	11	19
GCC	11	37	32	40
GCG	13	0	0	10
Ala GCT	39	47	55	27
GGA	46	3	8	24
GGC	8	54	54	36
GGG	5	3	3	25
Gly GGT	41	41	36	16
GTA	27	2	2	9
GTC	8	42	53	25
GTG	24	50	35	48
Val GTT	41	6	10	16
AAA	66	54	37	39
Lys AAG	34	46	63	61
AAC	27	59	57	58
Asn AAT	73	41	43	43
CAA	57	79	47	25
Gln CAG	43	21	53	76
CAC	46	54	31	59
His CAT	54	46	69	39
GAA	68	50	47	39
Glu GAG	32	50	53	61
GAC	23	54	46	56
Asp GAT	77	46	54	42
TAC	42	63	65	60
Tyr TAT	58	37	35	40
TGC	27	27	36	60
Cys TGT	73	73	64	41
TTC	44	60	48	58
Phe TTT	56	40	52	41
ATA	32	0	0	13
ATC	18	61	51	55
Ile ATT	50	39	49	34
Met ATG	100	100	100	100
Trp TGG	100	100	100	100

00645705-082400

Figure 5A

Codon Usage YG#81-6G01 (yellow-green)

TTT	Phe	14	TCT	Ser	7	TAT	Tyr	11	TGT	Cys	8
TTC	Phe	11	TCC	Ser	2	TAC	Tyr	8	TGC	Cys	3
TTA	Leu	17	TCA	Ser	6	TAA	***	0	TGA	***	0
TTG	Leu	13	TCG	Ser	7	TAG	***	0	TGG	Trp	2
CTT	Leu	12	CCT	Pro	9	CAT	His	7	CGT	Arg	5
CTC	Leu	4	CCC	Pro	8	CAC	His	6	CGC	Arg	1
CTA	Leu	5	CCA	Pro	9	CAA	Gln	8	CGA	Arg	7
CTG	Leu	4	CCG	Pro	2	CAG	Gln	6	CGG	Arg	0
ATT	Ile	19	ACT	Thr	8	AAT	Asn	16	AGT	Ser	7
ATC	Ile	7	ACC	Thr	2	AAC	Asn	6	AGC	Ser	2
ATA	Ile	12	ACA	Thr	10	AAA	Lys	23	AGA	Arg	6
ATG	Met	11	ACG	Thr	2	AAG	Lys	12	AGG	Arg	7
GTT	Val	20	GCT	Ala	15	GAT	Asp	20	GGT	Gly	16
GTC	Val	4	GCC	Ala	4	GAC	Asp	6	GGC	Gly	3
GTA	Val	13	GCA	Ala	14	GAA	Glu	26	GGA	Gly	18
GTG	Val	12	GCG	Ala	5	GAG	Glu	12	GGG	Gly	2

09645706-082400

Figure 5B

Codon Usage: GRver1

TTT	Phe	12	TCT	Ser	16	TAT	Tyr	9	TGT	Cys	5
TTC	Phe	13	TCC	Ser	0	TAC	Tyr	10	TGC	Cys	6
TTA	Leu	0	TCA	Ser	0	TAA	***	0	TGA	***	0
TTG	Leu	27	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	0	CCT	Pro	14	CAT	His	6	CGT	Arg	13
CTC	Leu	0	CCC	Pro	0	CAC	His	7	CGC	Arg	13
CTA	Leu	0	CCA	Pro	14	CAA	Gln	7	CGA	Arg	0
CTG	Leu	28	CCG	Pro	0	CAG	Gln	7	CGG	Arg	0
ATT	Ile	19	ACT	Thr	11	AAT	Asn	11	AGT	Ser	0
ATC	Ile	19	ACC	Thr	11	AAC	Asn	11	AGC	Ser	15
ATA	Ile	0	ACA	Thr	0	AAA	Lys	17	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	18	AGG	Arg	0
GTT	Val	0	GCT	Ala	18	GAT	Asp	13	GGT	Gly	19
GTC	Val	25	GCC	Ala	19	GAC	Asp	13	GGC	Gly	20
GTA	Val	0	GCA	Ala	0	GAA	Glu	19	GGA	Gly	0
GTG	Val	25	GCG	Ala	0	GAG	Glu	19	GGG	Gly	0

004280" 9075496

Figure 5C

Codon Usage: RDver1

TTT	Phe	13	TCT	Ser	15	TAT	Tyr	10	TGT	Cys	6
TTC	Phe	12	TCC	Ser	0	TAC	Tyr	10	TGC	Cys	5
TTA	Leu	0	TCA	Ser	0	TAA	***	0	TGA	***	0
TTG	Leu	27	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	0	CCT	Pro	14	CAT	His	7	CGT	Arg	13
CTC	Leu	1	CCC	Pro	0	CAC	His	6	CGC	Arg	13
CTA	Leu	0	CCA	Pro	14	CAA	Gln	8	CGA	Arg	0
CTG	Leu	27	CCG	Pro	0	CAG	Gln	7	CGG	Arg	0
ATT	Ile	20	ACT	Thr	11	AAT	Asn	10	AGT	Ser	0
ATC	Ile	19	ACC	Thr	11	AAC	Asn	11	AGC	Ser	15
ATA	Ile	0	ACA	Thr	0	AAA	Lys	18	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	17	AGG	Arg	0
GTT	Val	0	GCT	Ala	19	GAT	Asp	13	GGT	Gly	20
GTC	Val	24	GCC	Ala	18	GAC	Asp	13	GGC	Gly	19
GTA	Val	0	GCA	Ala	0	GAA	Glu	19	GGA	Gly	0
GTG	Val	25	GCG	Ala	0	GAG	Glu	19	GGG	Gly	0

004280" 90454960

Figure 5D

Codon Usage: Grver2

TTT	Phe	12	TCT	Ser	15	TAT	Tyr	9	TGT	Cys	5
TTC	Phe	13	TCC	Ser	0	TAC	Tyr	10	TGC	Cys	6
TTA	Leu	0	TCA	Ser	0	TAA	***	0	TGA	***	0
TTG	Leu	27	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	0	CCT	Pro	14	CAT	His	6	CGT	Arg	13
CTC	Leu	0	CCC	Pro	0	CAC	His	7	CGC	Arg	13
CTA	Leu	0	CCA	Pro	14	CAA	Gln	10	CGA	Arg	0
CTG	Leu	28	CCG	Pro	0	CAG	Gln	4	CGG	Arg	0
ATT	Ile	20	ACT	Thr	11	AAT	Asn	11	AGT	Ser	0
ATC	Ile	18	ACC	Thr	11	AAC	Asn	11	AGC	Ser	16
ATA	Ile	0	ACA	Thr	0	AAA	Lys	16	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	19	AGG	Arg	0
GTT	Val	0	GCT	Ala	18	GAT	Asp	13	GGT	Gly	18
GTC	Val	28	GCC	Ala	19	GAC	Asp	13	GGC	Gly	21
GTA	Val	0	GCA	Ala	0	GAA	Glu	17	GGA	Gly	0
GTG	Val	22	GCG	Ala	0	GAG	Glu	21	GGG	Gly	0

004280" 90454960

Figure 5E

Codon Usage:Rdver2

TTT	Phe	13	TCT	Ser	16	TAT	Tyr	10	TGT	Cys	6
TTC	Phe	12	TCC	Ser	0	TAC	Tyr	10	TGC	Cys	5
TTA	Leu	0	TCA	Ser	0	TAA	***	0	TGA	***	0
TTG	Leu	27	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	0	CCT	Pro	15	CAT	His	7	CGT	Arg	13
CTC	Leu	1	CCC	Pro	0	CAC	His	6	CGC	Arg	13
CTA	Leu	0	CCA	Pro	13	CAA	Gln	8	CGA	Arg	0
CTG	Leu	27	CCG	Pro	0	CAG	Gln	7	CGG	Arg	0
ATT	Ile	19	ACT	Thr	11	AAT	Asn	10	AGT	Ser	0
ATC	Ile	20	ACC	Thr	11	AAC	Asn	11	AGC	Ser	14
ATA	Ile	0	ACA	Thr	0	AAA	Lys	19	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	16	AGG	Arg	0
GTT	Val	0	GCT	Ala	19	GAT	Asp	13	GGT	Gly	21
GTC	Val	21	GCC	Ala	17	GAC	Asp	13	GGC	Gly	18
GTA	Val	0	GCA	Ala	1	GAA	Glu	21	GGA	Gly	0
GTG	Val	28	GCG	Ala	0	GAG	Glu	17	GGG	Gly	0

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Figure 5F

Codon Usage: GRver3

TTT	Phe	13	TCT	Ser	16	TAT	Tyr	9	TGT	Cys	7
TTC	Phe	12	TCC	Ser	0	TAC	Tyr	10	TGC	Cys	4
TTA	Leu	0	TCA	Ser	0	TAA	***	0	TGA	***	0
TTG	Leu	26	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	0	CCT	Pro	18	CAT	His	6	CGT	Arg	14
CTC	Leu	5	CCC	Pro	0	CAC	His	7	CGC	Arg	12
CTA	Leu	0	CCA	Pro	10	CAA	Gln	9	CGA	Arg	0
CTG	Leu	24	CCG	Pro	0	CAG	Gln	5	CGG	Arg	0
ATT	Ile	14	ACT	Thr	14	AAT	Asn	11	AGT	Ser	0
ATC	Ile	24	ACC	Thr	8	AAC	Asn	11	AGC	Ser	15
ATA	Ile	0	ACA	Thr	0	AAA	Lys	21	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	14	AGG	Arg	0
GTT	Val	1	GCT	Ala	18	GAT	Asp	12	GGT	Gly	18
GTC	Val	22	GCC	Ala	18	GAC	Asp	14	GGC	Gly	21
GTA	Val	0	GCA	Ala	1	GAA	Glu	20	GGA	Gly	0
GTG	Val	27	GCG	Ala	0	GAG	Glu	18	GGG	Gly	0

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Figure 5G

Codon Usage: RDver3

TTT	Phe	13	TCT	Ser	14	TAT	Tyr	7	TGT	Cys	6
TTC	Phe	12	TCC	Ser	1	TAC	Tyr	13	TGC	Cys	5
TTA	Leu	0	TCA	Ser	0	TAA	***	0	TGA	***	0
TTG	Leu	27	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	0	CCT	Pro	16	CAT	His	10	CGT	Arg	16
CTC	Leu	6	CCC	Pro	0	CAC	His	3	CGC	Arg	10
CTA	Leu	0	CCA	Pro	12	CAA	Gln	8	CGA	Arg	0
CTG	Leu	22	CCG	Pro	0	CAG	Gln	7	CGG	Arg	0
ATT	Ile	20	ACT	Thr	10	AAT	Asn	10	AGT	Ser	0
ATC	Ile	19	ACC	Thr	12	AAC	Asn	11	AGC	Ser	15
ATA	Ile	0	ACA	Thr	0	AAA	Lys	13	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	22	AGG	Arg	0
GTT	Val	0	GCT	Ala	20	GAT	Asp	14	GGT	Gly	16
GTC	Val	27	GCC	Ala	16	GAC	Asp	12	GGC	Gly	23
GTA	Val	0	GCA	Ala	1	GAA	Glu	18	GGA	Gly	0
GTG	Val	22	GCG	Ala	0	GAG	Glu	20	GGG	Gly	0

004280" 90454960

Figure 5H

Codon Usage: GRver4

TTT	Phe	11	TCT	Ser	13	TAT	Tyr	7	TGT	Cys	8
TTC	Phe	14	TCC	Ser	2	TAC	Tyr	12	TGC	Cys	3
TTA	Leu	0	TCA	Ser	1	TAA	***	0	TGA	***	0
TTG	Leu	21	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	1	CCT	Pro	18	CAT	His	7	CGT	Arg	14
CTC	Leu	11	CCC	Pro	0	CAC	His	6	CGC	Arg	11
CTA	Leu	0	CCA	Pro	10	CAA	Gln	11	CGA	Arg	1
CTG	Leu	22	CCG	Pro	0	CAG	Gln	3	CGG	Arg	0
ATT	Ile	13	ACT	Thr	14	AAT	Asn	11	AGT	Ser	1
ATC	Ile	25	ACC	Thr	8	AAC	Asn	11	AGC	Ser	14
ATA	Ile	0	ACA	Thr	0	AAA	Lys	20	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	15	AGG	Arg	0
GTT	Val	3	GCT	Ala	19	GAT	Asp	12	GGT	Gly	17
GTC	Val	22	GCC	Ala	15	GAC	Asp	14	GGC	Gly	19
GTA	Val	0	GCA	Ala	3	GAA	Glu	20	GGA	Gly	3
GTG	Val	25	GCG	Ala	0	GAG	Glu	18	GGG	Gly	0

004280 " 90254960

Figure 5I

Codon Usage: RDver4

TTT	Phe	13	TCT	Ser	11	TAT	Tyr	7	TGT	Cys	7
TTC	Phe	12	TCC	Ser	2	TAC	Tyr	13	TGC	Cys	4
TTA	Leu	0	TCA	Ser	2	TAA	***	0	TGA	***	0
TTG	Leu	28	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	0	CCT	Pro	16	CAT	His	11	CGT	Arg	15
CTC	Leu	7	CCC	Pro	2	CAC	His	2	CGC	Arg	11
CTA	Leu	0	CCA	Pro	10	CAA	Gln	7	CGA	Arg	0
CTG	Leu	20	CCG	Pro	0	CAG	Gln	8	CGG	Arg	0
ATT	Ile	21	ACT	Thr	11	AAT	Asn	10	AGT	Ser	1
ATC	Ile	18	ACC	Thr	11	AAC	Asn	11	AGC	Ser	14
ATA	Ile	0	ACA	Thr	0	AAA	Lys	13	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	22	AGG	Arg	0
GTT	Val	3	GCT	Ala	22	GAT	Asp	15	GGT	Gly	14
GTC	Val	27	GCC	Ala	11	GAC	Asp	11	GGC	Gly	21
GTA	Val	0	GCA	Ala	4	GAA	Glu	18	GGA	Gly	4
GTG	Val	19	GCG	Ala	0	GAG	Glu	20	GGG	Gly	0

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Figure 5J

Codon Usage: GRver5

TTT	Phe	10	TCT	Ser	11	TAT	Tyr	7	TGT	Cys	8
TTC	Phe	15	TCC	Ser	4	TAC	Tyr	12	TGC	Cys	3
TTA	Leu	0	TCA	Ser	1	TAA	***	0	TGA	***	0
TTG	Leu	23	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	1	CCT	Pro	17	CAT	His	6	CGT	Arg	13
CTC	Leu	12	CCC	Pro	2	CAC	His	7	CGC	Arg	11
CTA	Leu	0	CCA	Pro	9	CAA	Gln	11	CGA	Arg	2
CTG	Leu	19	CCG	Pro	0	CAG	Gln	3	CGG	Arg	0
ATT	Ile	15	ACT	Thr	14	AAT	Asn	9	AGT	Ser	1
ATC	Ile	23	ACC	Thr	8	AAC	Asn	13	AGC	Ser	14
ATA	Ile	0	ACA	Thr	0	AAA	Lys	19	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	16	AGG	Arg	0
GTT	Val	3	GCT	Ala	18	GAT	Asp	12	GGT	Gly	16
GTC	Val	21	GCC	Ala	14	GAC	Asp	14	GGC	Gly	21
GTA	Val	1	GCA	Ala	5	GAA	Glu	19	GGA	Gly	1
GTG	Val	25	GCG	Ala	0	GAG	Glu	19	GGG	Gly	1

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Figure 5K

Codon Usage: RDver5

TTT	Phe	13	TCT	Ser	12	TAT	Tyr	7	TGT	Cys	7
TTC	Phe	12	TCC	Ser	2	TAC	Tyr	13	TGC	Cys	4
TTA	Leu	0	TCA	Ser	2	TAA	***	0	TGA	***	0
TTG	Leu	25	TCG	Ser	0	TAG	***	0	TGG	Trp	2
CTT	Leu	1	CCT	Pro	15	CAT	His	9	CGT	Arg	14
CTC	Leu	11	CCC	Pro	1	CAC	His	4	CGC	Arg	12
CTA	Leu	0	CCA	Pro	12	CAA	Gln	7	CGA	Arg	0
CTG	Leu	18	CCG	Pro	0	CAG	Gln	8	CGG	Arg	0
ATT	Ile	19	ACT	Thr	10	AAT	Asn	9	AGT	Ser	2
ATC	Ile	20	ACC	Thr	11	AAC	Asn	12	AGC	Ser	12
ATA	Ile	0	ACA	Thr	1	AAA	Lys	13	AGA	Arg	0
ATG	Met	11	ACG	Thr	0	AAG	Lys	22	AGG	Arg	0
GTT	Val	5	GCT	Ala	21	GAT	Asp	14	GGT	Gly	14
GTC	Val	26	GCC	Ala	12	GAC	Asp	12	GGC	Gly	21
GTA	Val	1	GCA	Ala	4	GAA	Glu	18	GGA	Gly	3
GTG	Val	17	GCG	Ala	0	GAG	Glu	20	GGG	Gly	1

004280-904950

Figure 6

Synthetic oligos for engineered GR/RD genes
(All oligos listed 5' to 3')

Coding strand: 5' _____ (_____) n _____ 3'
Non-coding strand: 3' _____ (_____) n _____ 5'

Oligos with pRAM flanking sequence identical for GR/RD

1) coding strand upstream flanking

RAM-C1: ACGCCAGCCCAAGCTTAGGCCTGAGTGGC (SEQ ID NO:35)
RAM-C2: CTTAATTCTCCCATCCCCCTGTTGACAATTAATCATCGGCTCG (SEQ ID NO:36)
RAM-C3: TATAATGTGAGGAATTGCGAGCGGATAACAATTTACACA (SEQ ID NO:37)

2) coding strand downstream flanking

RAM-C4: ATGGGATGTTACCTAGACCAATATGAAATATTTGGTAAAT (SEQ ID NO:38)
RAM-C5: AAATGCTTAATGAATTTCAAAAAAAAAAAAAAGGAATTC (SEQ ID NO:39)
RAM-C6: GATATCAAGCTTATCGATACCGTCGACCTCGAGGATTATA (SEQ ID NO:40)
RAM-C7: TAGAAAAAGGCCTCGGCGGCCGCTAGTTCAGTCAGTT (SEQ ID NO:41)

3) non-coding strand downstream flanking

RAM-N1: AACTGACTGAACTAGCG (SEQ ID NO:42)
RAM-N2: GCCGCCGAGGCCTTTTTCTATATAATCCTCGAGGTCGACG (SEQ ID NO:43)
RAM-N3: GTATCGATAAGCTTGATATCGAATTCCTTTTTTTTTTTTTT (SEQ ID NO:44)
RAM-N3b: AGCTTGATATCGAATTCCTTTTTTTTTTTTTTTGAAATTC (SEQ ID NO:45)
RAM-N4: TTGAAATTCATTAAGCATTTATTTACCAAATATTTTCATAT (SEQ ID NO:46)
RAM-N5: TGGTCTAGGTAACATCCCATCACTAGCTTTTTTTTCTATA (SEQ ID NO:47)

4) non-coding strand upstream flanking

RAM-N6: TCGCAATTCCTCACATTATACGAGCCGATGATTAATTGTC (SEQ ID NO:48)
RAM-N7: AACAGGGGGATGGGGAGAATTAAGGCCACTCAGGCCTAAGCTTGGGCTGGCGT (SEQ ID NO:49)

GRver5 with flanking seq. of pRAM to end of *Sfi* I primers

1) Coding strand (Start and stop codons are underlined)

GR-C1: GGAAACAGGATCCCATGATGAAACGCGAAAAGAACGTGAT (SEQ ID NO:50)
GR-C2: CTACGGCCCAGAACCACTGCATCCACTGGAAGACCTCACC (SEQ ID NO:51)
GR-C3: GCTGGTGAGATGCTCTTCCGAGCACTGCGTAAACATAGTC (SEQ ID NO:52)
GR-C4: ACCTCCCTCAAGCACTCGTGGACGTCGTGGGAGACGAGAG (SEQ ID NO:53)
GR-C5: CCTCTCCTACAAAGAATTTTTCGAAGCTACTGTGCTGTTG (SEQ ID NO:54)
GR-C6: GCCCAAAGCCTCCATAATTGTGGGTACAAAATGAACGATG (SEQ ID NO:55)
GR-C7: TGGTGAGCATTTGTGCTGAGAATAAACACTCGCTTCTTTAT (SEQ ID NO:56)
GR-C8: TCCTGTAAATCGCTGCTTGGTACATCGGCATGATTGTCGCC (SEQ ID NO:57)
GR-C9: CCTGTGAATGAATCTTACATCCCAGATGAGCTGTGTAAGG (SEQ ID NO:58)
GR-C10: TTATGGGTATTAGCAAACCTCAAATCGTCTTTACTACCAA (SEQ ID NO:59)
GR-C11: AAACATCTTGAATAAGGTCTTGAAGTCCAGTCTCGTACT (SEQ ID NO:60)
GR-C12: AACTTCATCAAACGCATCATTATTCTGGATACCGTCGAAA (SEQ ID NO:61)
GR-C13: ACATCCACGGCTGTGAGAGCCTCCCTAACTTCATCTCTCG (SEQ ID NO:62)
GR-C14: TTACAGCGATGGTAATATCGCTAATTTCAAGCCCTTGCAT (SEQ ID NO:63)
GR-C15: TTTGATCCAGTCGAGCAAGTGGCCGCTATTTTGTGCTCCT (SEQ ID NO:64)
GR-C16: CCGGCAACCACTGGTTTGCCTAAAGGTGTCATGCAGACTCA (SEQ ID NO:65)
GR-C17: CCAGAATATCTGTGTGCGTTTGATCCACGCTCTCGACCCT (SEQ ID NO:66)
GR-C18: CGTGTGGGTACTCAATTGATCCCTGGCGTGACTGTGCTGG (SEQ ID NO:67)
GR-C19: TGTATCTGCCTTTCTTTACGCCTTTGGTTTCTCTATTAC (SEQ ID NO:68)
GR-C20: CCTGGGCTATTTTCATGGTCGGCTTGCCTGTCATCATGTTT (SEQ ID NO:69)

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Figure 6 (Cont.)

GR-C21: CGTCGCTTCGACCAAGAAGCCTTCTTGAAGGCTATTCAAG (SEQ ID NO:70)
 GR-C22: ACTACGAGGTGCGTTCCGTGATCAACGTCCCTTCAGTCAT (SEQ ID NO:71)
 GR-C23: TTTGTTCCCTGAGCAAATCTCCTTTGGTTGACAAGTATGATCTG (SEQ ID NO:72)
 GR-C24: AGCAGCTTGCGTGAGCTGTGCTGTGGCGCTGCTCCTT (SEQ ID NO:73)
 GR-C25: TGGCCAAAGAAGTGGCCGAGGTCGCTGCTAAGCGTCTGAA (SEQ ID NO:74)
 GR-C26: CCTCCCTGGTATCCGCTGCGGTTTTGGTTTGACTGAGAGC (SEQ ID NO:75)
 GR-C27: ACTTCTGCTAACATCCATAGCTTGCGAGACGAGTTTAAGT (SEQ ID NO:76)
 GR-C28: CTGGTAGCCTGGGTGCGGTGACTCCTCTTATGGCTGCAA (SEQ ID NO:77)
 GR-C29: GATCGCCGACCGTGAGACCGGCAAAGCACTGGGCCCAAAT (SEQ ID NO:78)
 GR-C30: CAAGTCGGTGAATTGTGTATTAAGGGCCCTATGGTCTCTA (SEQ ID NO:79)
 GR-C31: AAGGCTACGTGAACAATGTGGAGGCCACTAAAGAAGCCAT (SEQ ID NO:80)
 GR-C32: TGATGATGATGGCTGGCTCCATAGCGGCGACTTCGGTTAC (SEQ ID NO:81)
 GR-C33: TATGATGAGGACGAACACTTCTATGTGGTCGATCGCTACA (SEQ ID NO:82)
 GR-C34: AAGAATTGATTAAGTACAAAGGCTCTCAAGTCGACCAGC (SEQ ID NO:83)
 GR-C35: CGAACTGGAAGAAATTTTGCTGAAGAACCCTTGATCCGC (SEQ ID NO:84)
 GR-C36: GACGTGGCCGTCGTGGGTATCCCAGACTTGGAAGCTGGCG (SEQ ID NO:85)
 GR-C37: AGTTGCCTAGCGCCTTTGTGGTGAAACAACCCGGCAAGGA (SEQ ID NO:86)
 GR-C38: GATCACTGCTAAGGAGGTCTACGACTATTTGGCCGAGCGC (SEQ ID NO:87)
 GR-C39: GTGTCTCACACCAAATATCTGCGTGGCGGCGTCCGCTTCG (SEQ ID NO:88)
 GR-C40: TCGATTCTATTCCACGCAACGTTACCGGTAAGATCACTCG (SEQ ID NO:89)
 GR-C41: TAAAGAGTTGCTGAAGCAACTCCTCGAAAAAGCTGGCGGC (SEQ ID NO:90)
 GR-C42: TAGTAAAGTCTTCATGATTATATAGAAAAAAGCTAGTG (SEQ ID NO:91)

2) non-coding strand

GR-N1: TAATCATGAAGACTTTACTAGCCGCCAGCTTTTTTCGAGGA (SEQ ID NO:92)
 GR-N2: GTTGCTTCAGCAACTCTTTACGAGTGATCTTACCGGTAAC (SEQ ID NO:93)
 GR-N3: GTTGCGTGGAATAGAATCGACGAAGCGGACGCCGCCACG (SEQ ID NO:94)
 GR-N4: CAGATATTTGGTGTGAGACACGCGCTCGGCCAAATAGTCGT (SEQ ID NO:95)
 GR-N5: AGACCTCCTTAGCAGTGATCTCCTTGCCGGGTTGTTTCAC (SEQ ID NO:96)
 GR-N6: CACAAAGGCGCTAGGCAACTCGCCAGCTTCCAAGTCTGGG (SEQ ID NO:97)
 GR-N7: ATACCCACGACGGCCACGTCGCGGATACAAGGGTTCTTCA (SEQ ID NO:98)
 GR-N8: GCAAAATTTCTTCCAGTTCGGCTGGTGC GACTTGAGAGCC (SEQ ID NO:99)
 GR-N9: TTTGTACTTAATCAATTCTTTGTAGCGATCGACCACATAG (SEQ ID NO:100)
 GR-N10: AAGTGTTCGTCCTCATCATAGTAACCGAAGTCGCCGCTAT (SEQ ID NO:101)
 GR-N11: GGAGCCAGCCATCATCATCAATGGCTTCTTTAGTGGCCTC (SEQ ID NO:102)
 GR-N12: CACATTGTTACGCTAGCCTTTAGAGACCATAGGGCCCTTA (SEQ ID NO:103)
 GR-N13: ATACACAATTCACCGACTTGATTTGGGCCAGTGCTTTGC (SEQ ID NO:104)
 GR-N14: CGGTCTCACGGTCGGCGATCTTTGCAGCCATAAGAGGAGT (SEQ ID NO:105)
 GR-N15: CACGCGACCCAGGCTACCAGACTTAAACTCGTCTCGCAAG (SEQ ID NO:106)
 GR-N16: CTATGGATGTTAGCAGAAGTGCTCTCAGTCAAACCAAAAC (SEQ ID NO:107)
 GR-N17: CGCAGCGGATACCAGGGAGGTTAGACGCTTAGCAGCGAC (SEQ ID NO:108)
 GR-N18: CTCGGCCACTTCTTTGGCCAAAGGAGCAGCGCCACAGCAC (SEQ ID NO:109)
 GR-N19: AGCTCACGCAAGCTGCTCAGATCATACTTGTC AACC AAAG (SEQ ID NO:110)
 GR-N20: GAGATTTGCTCAGGAACAAATGACTGAAGGGACGTTGAT (SEQ ID NO:111)
 GR-N21: CACGGAACGCACCTCGTAGTCTTGAATAGCCTTCAA (SEQ ID NO:112)
 GR-N22: GAAGGCTTCTTGGTGAAGCGACGAAACATGATGACACGCAAGC (SEQ ID NO:113)
 GR-N23: CGACCATGAAATAGCCCAGGGTAATAGAGAAACCAAAGGC (SEQ ID NO:114)
 GR-N24: GTGAAAGAAAGGCAGATACACCAGCACAGTCACGCCAGGG (SEQ ID NO:115)
 GR-N25: ATCAATTGAGTACCCACACGAGGGTCGAGAGCGTGGATCA (SEQ ID NO:116)
 GR-N26: AACGCACACAGATATTCTGGTGAGTCTGCATGACACCTTT (SEQ ID NO:117)
 GR-N27: AGGCAAACCAAGTGGTGCCGGAGGAGCACAAATAGCGGCC (SEQ ID NO:118)

Figure 6 (Cont.)

GR-N28:ACTTGCTCGACTGGATCAAAATGCAAGGGCTTGAAATTAG (SEQ ID NO:119)
 GR-N29:CGATATTACCATCGCTGTAACGAGAGATGAAGTTAGGGAG (SEQ ID NO:120)
 GR-N30:GCTCTCACAGCCGTGGATGTTTTTCGACGGTATCCAGAATA (SEQ ID NO:121)
 GR-N31:ATGATGCGTTTTGATGAAGTTAGTACGAGACTGGACTTCCA (SEQ ID NO:122)
 GR-N32:AGACCTTATTCAAGATGTTTTTGGTAGTAAAGACGATTTG (SEQ ID NO:123)
 GR-N33:AGGTTTGCTAATACCCATAACCTTACACAGCTCATCTGGG (SEQ ID NO:124)
 GR-N34:ATGTAAGATTTCATTCACAGGGGCGACAATCATGCCGATGT (SEQ ID NO:125)
 GR-N35:ACCAAGCAGCGATTACAGGAATAAAGAAGCGAGTGTATT (SEQ ID NO:126)
 GR-N36:CTCAGCACAAATGCTCACCACATCGTTCATTTTGTACCCA (SEQ ID NO:127)
 GR-N37:CAATTATGGAGGCTTTGGGCCAACAGCACAGTAGCTTCGA (SEQ ID NO:128)
 GR-N38:AAAATTCTTTGTAGGAGAGGCTCTCGTCTCCACGACGTC (SEQ ID NO:129)
 GR-N39:CACGAGTGCTTGAGGGAGGTGACTATGTTTACGCAGTGCT (SEQ ID NO:130)
 GR-N40:CGGAAGAGCATCTCACCAGCGGTGAGGTCTTCCAGTGGAT (SEQ ID NO:131)
 GR-N41:GCAGTGGTTCTGGGCCGTAGATCACGTTCTTTTCGCGTTT (SEQ ID NO:132)
 GR-N42:CATCATGGGATCCTGTTTCCTGTGTGAAATTGTTATCCGC (SEQ ID NO:133)

RDver5 with flanking sequence of pRAM to end of *Sfi* I primers

1) coding strand

RD-C1: GGAAACAGGATCCCATGATGAAGCGTGAGAAAAATGTCAT (SEQ ID NO:134)
 RD-C2: CTATGGCCCTGAGCCTCTCCATCCTTTGGAGGATTTGACT (SEQ ID NO:135)
 RD-C3: GCCGGCGAAATGCTGTTTCGTGCTCTCCGCAAGCACTCTC (SEQ ID NO:136)
 RD-C4: ATTTGCCTCAAGCCTTGGTCGATGTGGTCGGCGATGAATC (SEQ ID NO:137)
 RD-C5: TTTGAGCTACAAGGAGTTTTTTGAGGCAACCGTCTTGCTG (SEQ ID NO:138)
 RD-C6: GCTCAGTCCCTCCACAATTGTGGCTACAAGATGAACGACG (SEQ ID NO:139)
 RD-C7: TCGTTAGTATCTGTGCTGAAAACAATACCCGTTTCTTCAT (SEQ ID NO:140)
 RD-C8: TCCAGTCATCGCCGATGGTATATCGGTATGATCGTGGCT (SEQ ID NO:141)
 RD-C9: CCAGTCAACGAGAGCTACATTCCCGACGAAGTGTGTAAG (SEQ ID NO:142)
 RD-C10:TCATGGGTATCTCTAAGCCACAGATTGTCTTCACCACTAA (SEQ ID NO:143)
 RD-C11:GAATATTCTGAACAAAGTCCTGGAAGTCCAAAGCCGCACC (SEQ ID NO:144)
 RD-C12:AACTTTATTAAAGCGTATCATCATCTTGGACACTGTGGAGA (SEQ ID NO:145)
 RD-C13:ATATTCACGGTTGCGAATCTTTGCCTAATTTTCATCTCTCG (SEQ ID NO:146)
 RD-C14:CTATTCAGACGGCAACATCGCAAACTTTAAACCACTCCAC (SEQ ID NO:147)
 RD-C15:TTGACCCCTGTGGAACAAGTTGCAGCCATTCTGTGTAGCA (SEQ ID NO:148)
 RD-C16:GCGGTACTACTGGACTCCCAAAGGGAGTCATGCAGACCCA (SEQ ID NO:149)
 RD-C17:TCAAAACATTTGCGTGCGTCTGATCCATGCTCTCGATCCA (SEQ ID NO:150)
 RD-C18:CGCTACGGCACTCAGCTGATTCTCGGTGTACCGTCTTGG (SEQ ID NO:151)
 RD-C19:TCTACTTGCCTTTCTTCCATGCTTTTCGGCTTTCATATTAC (SEQ ID NO:152)
 RD-C20:TTTGGGTTACTTTATGGTCGGTCTCCGCGTGATTATGTTT (SEQ ID NO:153)
 RD-C21:CGCCGTTTGTATCAGGAGGCTTTCTTGAAAGCCATCCAAG (SEQ ID NO:154)
 RD-C22:ATTATGAAGTCCGCAAGTGTATCAACGTGCCTAGCGTGAT (SEQ ID NO:155)
 RD-C23:CCTGTTTTTGTCTAAGAGCCCACTCGTGGACAAGTACGAC (SEQ ID NO:156)
 RD-C24:TTGTCTTCACTGCGTGAATTGTGTTGCGGTGCCGCTCCAC (SEQ ID NO:157)
 RD-C25:TGGCTAAGGAGGTCGCTGAAGTGGCCGCCAAACGCTTGAA (SEQ ID NO:158)
 RD-C26:TCTTCCAGGGATTCTGTTGTGGCTTTCGGCTCACCGAATCT (SEQ ID NO:159)
 RD-C27:ACCAGCGCTATTATTTCAGTCTCTCCGCGATGAGTTTAAGA (SEQ ID NO:160)
 RD-C28:GCGGCTCTTTGGGCCGTGTCACTCCACTCATGGCTGCTAA (SEQ ID NO:161)
 RD-C29:GATCGCTGATCGCGAACTGGTAAGGCTTTGGGCCCTAAC (SEQ ID NO:162)
 RD-C30:CAAGTGGGCGAGCTGTGTATCAAAGGCCCTATGGTGAGCA (SEQ ID NO:163)
 RD-C31:AGGGTTATGTCAATAACGTGGAAGCTACCAAGGAGGCCAT (SEQ ID NO:164)
 RD-C32:CGACGACGACGGCTGGTTGCATTCTGGTGATTTTGGATAT (SEQ ID NO:165)
 RD-C33:TACGACGAAGATGAGCATTTTACGTGCTGGATCGTTACA (SEQ ID NO:166)
 RD-C34:AGGAGCTGATCAAATACAAGGGTAGCCAGGTTGCTCCAGC (SEQ ID NO:167)
 RD-C35:TGAGTTGGAGGAGATTCTGTTGAAAAATCCATGCATTTCGC (SEQ ID NO:168)

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Figure 6 (Cont.)

RD-C36: GATGTCGCTGTGGTCGGCATTCTGATCTGGAGGCCGGCG (SEQ ID NO:169)
RD-C37: AACTGCCTTCTGCTTTCGTTGTCAAGCAGCCTGGTAAAGA (SEQ ID NO:170)
RD-C38: AATTACCGCCAAAGAAGTGTATGATTACCTGGCTGAACGT (SEQ ID NO:171)
RD-C39: GTGAGCCATACTAAGTACTTGGCGTGGCGGCGTGCCTTTTG (SEQ ID NO:172)
RD-C40: TTGACTCCATCCCTCGTAACGTAACAGGCAAAATTACCCG (SEQ ID NO:173)
RD-C41: CAAGGAGCTGTTGAAACAATTGTTGGAGAAAGGCCGGCGGT (SEQ ID NO:174)
RD-C42: TAGTAAAGTCTTCATGATTATATAGAAAAAAGCTAGTG (SEQ ID NO:175)

2) non-coding strand

RD-N1: TAATCATGAAGACTTTACTAACCGCCGGCCTTCTCCAACA (SEQ ID NO:176)
RD-N2: ATTGTTTCAACAGCTCCTTGCGGGTAATTTTGCCTGTTAC (SEQ ID NO:177)
RD-N3: GTTACGAGGGATGGAGTCAACAAAACGCACGCCGCCACGC (SEQ ID NO:178)
RD-N4: AAGTACTTAGTATGGCTCACACGTTTCAGCCAGGTAATCAT (SEQ ID NO:179)
RD-N5: ACACTTCTTTGGCGGTAATTTCTTTACCAGGCTGCTTGAC (SEQ ID NO:180)
RD-N6: AACGAAAGCAGAAGGCAGTTTCGCCGGCCTCCAGATCAGGA (SEQ ID NO:181)
RD-N7: ATGCCGACCACAGCGACATCGCGAATGCATGGATTTTTCA (SEQ ID NO:182)
RD-N8: ACAGAATCTCCTCCAACCTCAGCTGGAGCAACCTGGCTACC (SEQ ID NO:183)
RD-N9: CTTGTATTTGATCAGCTCCTTGTAACGATCCACGACGTAA (SEQ ID NO:184)
RD-N10: AAATGCTCATCTTCGTCGTAATATCCAAAATCACCAGAAT (SEQ ID NO:185)
RD-N11: GCAACCAGCCGTCGTCGTCGATGGCCTCCTTGGTAGCTTC (SEQ ID NO:186)
RD-N12: GACGTTATTGACATAACCCCTTGCTCACCATAGGGCCTTTG (SEQ ID NO:187)
RD-N13: ATACACAGCTCGCCCACTTGGTTAGGGCCCAAAGCCTTAC (SEQ ID NO:188)
RD-N14: CAGTTTCGCGATCAGCGATCTTAGCAGCCATGAGTGGAGT (SEQ ID NO:189)
RD-N15: GACACGGCCCAAAGAGCCGCTCTTAAACTCATCGCGGAGA (SEQ ID NO:190)
RD-N16: GACTGAATAATAGCGCTGGTAGATTTCGGTGAGGCCGA (SEQ ID NO:191)
RD-N17: AGCCACAACGAATCCCTGGAAGATTCAAGCGTTTGGCGGCCAC (SEQ ID NO:192)
RD-N18: TTCAGCGACCTCCTTAGCCAGTGGAGCGGCACCGCAACAC (SEQ ID NO:193)
RD-N19: AATTCACGCAGTGAAGACAAGTCGTACTTGTCCACGAGTG (SEQ ID NO:194)
RD-N20: GGCTCTTAGACAAAAACAGGATCACGCTAGGCACGTTGAT (SEQ ID NO:195)
RD-N21: GACACTGCGGACTTCATAATCTTGGATGGCTTTCAAGAAA (SEQ ID NO:196)
RD-N22: GCCTCCTGATCAAAACGGCGGAACATAATCACGCGGAGAC (SEQ ID NO:197)
RD-N23: CGACCATAAAGTAACCCAAAGTAATATGAAAGCCGAAAGC (SEQ ID NO:198)
RD-N24: ATGGAAGAAAGGCAAGTAGACCAAGACGGTGACACCAGGA (SEQ ID NO:199)
RD-N25: ATCAGCTGAGTGCCGTAGCGTGGATCGAGAGCATGGATCA (SEQ ID NO:200)
RD-N26: GACGCACGCAAATGTTTTGATGGGTCTGCATGACTCCCTT (SEQ ID NO:201)
RD-N27: TGGGAGTCCAGTAGTACCGCTGCTACACAGAATGGCTGCA (SEQ ID NO:202)
RD-N28: ACTTGTTCCACAGGGTCGAAGTGGAGTGGTTTAAAGTTTG (SEQ ID NO:203)
RD-N29: CGATGTTGCCGTCTGAATAGCGAGAGATGAAATTAGGCAA (SEQ ID NO:204)
RD-N30: AGATTTCGCAACCGTGAATATTCTCCACAGTGTCCAAGATG (SEQ ID NO:205)
RD-N31: ATGATACGCTTAATAAAGTTGGTGCGGCTTTGGACTTCCA (SEQ ID NO:206)
RD-N32: GGACTTTGTTTCCAGAAATATTCTTAGTGGTGAAGACAATCTG (SEQ ID NO:207)
RD-N33: TGGCTTAGAGATACCCATGACTTTACACAGTTTCGTCGGGA (SEQ ID NO:208)
RD-N34: ATGTAGCTCTCGTTGACTGGAGCCACGATCATACCGATAT (SEQ ID NO:209)
RD-N35: ACCATGCGGCGATGACTGGAATGAAGAAACGGGTATTGTT (SEQ ID NO:210)
RD-N36: TTCAGCACAGATACTAACGACGTCGTTTCATCTTGTAGCCA (SEQ ID NO:211)
RD-N37: CAATTGTGGAGGGACTGAGCCAGCAAGACGGTTGCCTCAA (SEQ ID NO:212)
RD-N38: AAAACTCCTTGTAGCTCAAAGATTATCGCCGACCACATC (SEQ ID NO:213)
RD-N39: GACCAAGGCTTGAGGCAATGAGAGTGCTTGGCGGAGAGCA (SEQ ID NO:214)
RD-N40: CGAAACAGCATTTTCGCCGCGAGTCAAATCCTCCAAAGGAT (SEQ ID NO:215)
RD-N41: GGAGAGGCTCAGGGCCATAGATGACATTTTTCTCACGCTT (SEQ ID NO:216)
RD-N42: CATCATGGGATCCTGTTTCCTGTGTGAAATTGTTATCCGC (SEQ ID NO:217)

Figure 7

RELLUC.SEQ A T G A C T T C A A G T T T A T G A T C C A G A A C A G G A A A C G G A 40
RLUCVER1.SEQ A T G G C T T C C A A G G T G T A C G A C C C G A G C A G C G C A A G C G C A 40
RLUCVER2.SEQ A T G G C T T C C A A G G T G T A C G A C C C G A G C A A C G C A A A C G C A 40
RLUCFINL.SEQ A T G G C T T C C A A G G T G T A C G A C C C G A G C A A C G C A A A C G C A 40

RELLUC.SEQ T G A T A A C T G G T C C G C A G T G G T G G G C C A G A T G T A A A C A A A T 80
RLUCVER1.SEQ T G A T C A C C G G C C C T C A G T G G T G G G C C G G C T G C A A G C A G A T 80
RLUCVER2.SEQ T G A T C A C T G G G C C T C A G T G G T G G G C T C G C T G C A A G C A A A T 80
RLUCFINL.SEQ T G A T C A C T G G G C C T C A G T G G T G G G C T C G C T G C A A G C A A A T 80

RELLUC.SEQ G A A T G T T C T T G A T T C A T T T A T T A A T T A T T A T G A T T C A G A A 120
RLUCVER1.SEQ G A A C G T G C T G G A C T C C T T C A T C A A C T A C T A C G A C A G C G A G 120
RLUCVER2.SEQ G A A C G T G C T G G A C T C C T T C A T C A A C T A C T A T G A T T C C G A G 120
RLUCFINL.SEQ G A A C G T G C T G G A C T C C T T C A T C A A C T A C T A T G A T T C C G A G 120

RELLUC.SEQ A A A C A T G C A G A A A A T G C T G T T A T T T T T T A C A T G G T A A C G 160
RLUCVER1.SEQ A A G C A C G C C G A G A A C G C C G T G A T C T T C C T G C A C G G C A A C G 160
RLUCVER2.SEQ A A G C A C G C C G A G A A C G C C G T G A T T T T T C T G C A T G G T A A C G 160
RLUCFINL.SEQ A A G C A C G C C G A G A A C G C C G T G A T T T T T C T G C A T G G T A A C G 160

RELLUC.SEQ C G G C C T C T T C T T A T T T A T G G C G A C A T G T T G T G C C A C A T A T 200
RLUCVER1.SEQ C G C C T C C A G C T A C C T G T G G A G G C A C G T G G T G C C T C A C A T 200
RLUCVER2.SEQ C T G C C T C C A G C T A C C T G T G G A G G C A C G T C G T G C C T C A C A T 200
RLUCFINL.SEQ C T G C C T C C A G C T A C C T G T G G A G G C A C G T C G T G C C T C A C A T 200

RELLUC.SEQ T G A G C C A G T A G C G C G G T G T A T T A T A C C A G A T C T T A T T G G T 240
RLUCVER1.SEQ C G A G C C C G T G G C C G C T G C A T C A T C C C T G A C C T G A T C G G C 240
RLUCVER2.SEQ C G A G C C C G T G G C T C G C T G C A T C A T C C C T G A T C T G A T C G G A 240
RLUCFINL.SEQ C G A G C C C G T G G C T A G A T G C A T C A T C C C T G A T C T G A T C G G A 240

RELLUC.SEQ A T G G G C A A A T C A G G C A A A T C T G G T A A T G G T T C T T A T A G G T 280
RLUCVER1.SEQ A T G G G C A A G T C C G G C A A G A G C G G C A A C G G C T C C T A C C G C C 280
RLUCVER2.SEQ A T G G G T A A G T C C G G C A A G A G C G G G A A T G G C T C A T A T C G C C 280
RLUCFINL.SEQ A T G G G T A A G T C C G G C A A G A G C G G G A A T G G C T C A T A T C G C C 280

RELLUC.SEQ T A C T T G A T C A T T A C A A A T A T C T T A C T G C A T G G T T T G A A C T 320
RLUCVER1.SEQ T G C T G G A C C A C T A C A A G T A C C T G A C C G C C T G G T T C G A G C T 320
RLUCVER2.SEQ T C C T G G A T C A C T A C A A G T A C C T C A C C G C T T G G T T C G A G C T 320
RLUCFINL.SEQ T C C T G G A T C A C T A C A A G T A C C T C A C C G C T T G G T T C G A G C T 320

RELLUC.SEQ T C T T A A T T T A C C A A A G A A G A T C A T T T T T G T C G G C C A T G A T 360
RLUCVER1.SEQ G C T G A A C C T G C C C A A G A A G A T C A T C T T C G T G G G C C A C G A C 360
RLUCVER2.SEQ G C T G A A C C T T C C A A A G A A A A T C A T C T T T G T G G G C C A C G A C 360
RLUCFINL.SEQ G C T G A A C C T T C C A A A G A A A A T C A T C T T T G T G G G C C A C G A C 360

RELLUC.SEQ T G G G G T G C T T G T T T G G C A T T T C A T T A T A G C T A T G A G C A T C 400
RLUCVER1.SEQ T G G G G A G C C T G C C T G G C C T T C C A C T A C T C C T A C G A G C A C C 400
RLUCVER2.SEQ T G G G G G C T T G T C T G G C C T T T C A C T A C T C C T A C G A G C A C C 400
RLUCFINL.SEQ T G G G G G C T T G T C T G G C C T T T C A C T A C T C C T A C G A G C A C C 400

RELLUC.SEQ A A G A T A A G A T C A A A G C A A T A G T T C A C G C T G A A A G T G T A G T 440
RLUCVER1.SEQ A G A C A A G A T C A A G G C C A T C G T G C A C G C C G A G A G C G T G G T 440
RLUCVER2.SEQ A A G A C A A G A T C A A G G C C A T C G T C C A T G C T G A G A G T G T C G T 440
RLUCFINL.SEQ A A G A C A A G A T C A A G G C C A T C G T C C A T G C T G A G A G T G T C G T 440

Figure 7 (Cont.)

RELLUC.SEQ A G A T G T G A T G A A T C A T G G G A T G A A T G G T G A T A T T G A A 480
 RLUCVER1.SEQ G G A C G T G A T C G A G T C C T G G G A C G A G T G G C C T G A C A T C G A G 480
 RLUCVER2.SEQ G G A C G T G A T C G A G T C C T G G G A C G A G T G G C C T G A C A T C G A G 480
 RLUCFINL.SEQ G G A C G T G A T C G A G T C C T G G G A C G A G T G G C C T G A C A T C G A G 480

RELLUC.SEQ G A A G A T A T T G C G T T G A T C A A A T C T G A A G A A G G A G A A A A A 520
 RLUCVER1.SEQ G A G A C A T C G C C C T G A T C A A G A G C G A G G A G G C G A G A A G A 520
 RLUCVER2.SEQ G A G A T A T C G C C C T G A T C A A G A G C G A A G A G G C G A G A A A A 520
 RLUCFINL.SEQ G A G A T A T C G C C C T G A T C A A G A G C G A A G A G G C G A G A A A A 520

RELLUC.SEQ T G G T T T T G G A G A A T A A C T T C T T C G T G G A A A C C A T G T T G C C 560
 RLUCVER1.SEQ T G G T G C T G G A G A A C A A C T T C T T C G T G G A G A C C A T G C T G C C 560
 RLUCVER2.SEQ T G G T G C T T G A G A A T A A C T T C T T C G T C G A G A C C A T G C T C C C 560
 RLUCFINL.SEQ T G G T G C T T G A G A A T A A C T T C T T C G T C G A G A C C A T G C T C C C 560

RELLUC.SEQ A T C A A A A A T C A T G A G A A A G T T A G A A C C A G A A G A A T T T G C A 600
 RLUCVER1.SEQ C A G C A A G A T C A T G C G C A A G C T G G A G C C T G A G G A G T T C G C C 600
 RLUCVER2.SEQ A A G C A A G A T C A T G C G G A A A C T G G A G C C T G A G G A G T T C G C T 600
 RLUCFINL.SEQ A A G C A A G A T C A T G C G G A A A C T G G A G C C T G A G G A G T T C G C T 600

RELLUC.SEQ G C A T A T C T T G A A C C A T T C A A A G A G A A A G G T G A A G T T C G T C 640
 RLUCVER1.SEQ G C T A C C T G G A G C C C T T C A A G G A G A A G G G C G A G G T G C G C C 640
 RLUCVER2.SEQ G C T A C C T G G A G C C C T T C A A G G A G A A G G G C G A G G T T A G A C 640
 RLUCFINL.SEQ G C T A C C T G G A G C C A T T C A A G G A G A A G G G C G A G G T T A G A C 640

RELLUC.SEQ G T C C A A C A T T A T C A T G G C C T C G T G A A A T C C C G T T A G T A A A 680
 RLUCVER1.SEQ G C C C T A C C C T G T C C T G G C C C C G C G A G A T C C C T C T G G T G A A 680
 RLUCVER2.SEQ G G C C T A C C C T C T C C T G G C C T C G C G A G A T C C C T C T C G T T A A 680
 RLUCFINL.SEQ G G C C T A C C C T C T C C T G G C C T C G C G A G A T C C C T C T C G T T A A 680

RELLUC.SEQ A G G T G G T A A A C C T G A C G T T G T A C A A A T T G T T A G G A A T T A T 720
 RLUCVER1.SEQ G G G C G G C A A G C C C G A C G T G G T G C A G A T C G T G C G C A A C T A C 720
 RLUCVER2.SEQ G G G A G G C A A G C C C G A C G T C G T C C A G A T T G T C C G C A A C T A C 720
 RLUCFINL.SEQ G G G A G G C A A G C C C G A C G T C G T C C A G A T T G T C C G C A A C T A C 720

RELLUC.SEQ A A T G C T T A T C T A C G T G C A A G T G A T G A T T T A C C A A A A A T G T 760
 RLUCVER1.SEQ A A C G C C T A C C T G C G C G C C A G C G A C G A C C T G C C T A A G A T G T 760
 RLUCVER2.SEQ A A C G C C T A C C T T C G G G C C A G C G A C G A T C T G C C T A A G A T G T 760
 RLUCFINL.SEQ A A C G C C T A C C T T C G G G C C A G C G A C G A T C T G C C T A A G A T G T 760

RELLUC.SEQ T T A T T G A A T C G G A T C C A G G A T T C T T T T C C A A T G C T A T T G T 800
 RLUCVER1.SEQ T C A T C G A G T C C G A C C C T G G C T T C T T T C C A A C G C C A T C G T 800
 RLUCVER2.SEQ T C A T C G A G T C C G A C C C T G G G T T C T T T T C C A A C G C T A T T G T 800
 RLUCFINL.SEQ T C A T C G A G T C C G A C C C T G G G T T C T T T T C C A A C G C T A T T G T 800

RELLUC.SEQ T G A A G G C G C C A A G A A G T T T C C T A A T A C T G A A T T T G T C A A A 840
 RLUCVER1.SEQ C G A G G G A G C C A A G A A G T T C C C C A A C A C C G A G T T C G T G A A G 840
 RLUCVER2.SEQ C G A G G G A G C T A A G A A G T T C C C T A A C A C C G A G T T C G T G A A G 840
 RLUCFINL.SEQ C G A G G G A G C T A A G A A G T T C C C T A A C A C C G A G T T C G T G A A G 840

RELLUC.SEQ G T A A A A G G T C T T C A T T T T T C G C A A G A A G A T G C A C C T G A T G 880
 RLUCVER1.SEQ G T G A A G G G C C T G C A C T T C T C C A G G A G G A C G C C C C T G A C G 880
 RLUCVER2.SEQ G T G A A G G G C C T C C A C T T C A G C C A G G A G G A C G C C C C A G A T G 880
 RLUCFINL.SEQ G T G A A G G G C C T C C A C T T C A G C C A G G A G G A C G C C C C A G A T G 880

Figure 7 (Cont.)

RELLUC.SEQ A A A T G G G A A T A T A T C A A A T C G T T C G T A G C G A G T T C T 920
 RLUCVER1.SEQ A G A T G G G C A A G T A C A T C A A G A G C T T C G T G G A G C G C G T G C T 920
 RLUCVER2.SEQ A A A T G G G T A A G T A C A T C A A G A G C T T C G T G G A G C G C G T G C T 920
 RLUCFINL.SEQ A A A T G G G T A A G T A C A T C A A G A G C T T C G T G G A G C G C G T G C T 920

RELLUC.SEQ C A A A A A T G A A C A A 933
 RLUCVER1.SEQ G A A G A A C G A G C A G 933
 RLUCVER2.SEQ G A A G A A C G A G C A G 933
 RLUCFINL.SEQ G A A G A A C G A G C A G 933

004280" 90254960

Figure 8

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RELLUC.SEQ  M T S K V Y D P E Q R K R M I T G P Q W W A R C K Q M N D S F I N Y Y D S E 118
RLUCVER1.SEQ M A S K V Y D P E Q R K R M I T G P Q W W A R C K Q M N V L D S F I N Y Y D S E 118
RLUCVER2.SEQ M A S K V Y D P E Q R K R M I T G P Q W W A R C K Q M N V L D S F I N Y Y D S E 118
RLUCFINL.SEQ M A S K V Y D P E Q R K R M I T G P Q W W A R C K Q M N V L D S F I N Y Y D S E 118

RELLUC.SEQ  K H A E N A V I F L H G N A A S S Y L W R H V V P H I E P V A R C I I P D L I G 238
RLUCVER1.SEQ K H A E N A V I F L H G N A A S S Y L W R H V V P H I E P V A R C I I P D L I G 238
RLUCVER2.SEQ K H A E N A V I F L H G N A A S S Y L W R H V V P H I E P V A R C I I P D L I G 238
RLUCFINL.SEQ K H A E N A V I F L H G N A A S S Y L W R H V V P H I E P V A R C I I P D L I G 238

RELLUC.SEQ  M G K S G K S G N G S Y R L L D H Y K Y L T A W F E L L N L P K K I I F V G H D 358
RLUCVER1.SEQ M G K S G K S G N G S Y R L L D H Y K Y L T A W F E L L N L P K K I I F V G H D 358
RLUCVER2.SEQ M G K S G K S G N G S Y R L L D H Y K Y L T A W F E L L N L P K K I I F V G H D 358
RLUCFINL.SEQ M G K S G K S G N G S Y R L L D H Y K Y L T A W F E L L N L P K K I I F V G H D 358

RELLUC.SEQ  W G A C L A F H Y S Y E H Q D K I K A I V H A E S V V D V I E S W D E W P D I E 478
RLUCVER1.SEQ W G A C L A F H Y S Y E H Q D K I K A I V H A E S V V D V I E S W D E W P D I E 478
RLUCVER2.SEQ W G A C L A F H Y S Y E H Q D K I K A I V H A E S V V D V I E S W D E W P D I E 478
RLUCFINL.SEQ W G A C L A F H Y S Y E H Q D K I K A I V H A E S V V D V I E S W D E W P D I E 478

RELLUC.SEQ  E D I A L I K S E E G E K M V L E N N F F V E T M L P S K I M R K L E P E E F A 598
RLUCVER1.SEQ E D I A L I K S E E G E K M V L E N N F F V E T M L P S K I M R K L E P E E F A 598
RLUCVER2.SEQ E D I A L I K S E E G E K M V L E N N F F V E T M L P S K I M R K L E P E E F A 598
RLUCFINL.SEQ E D I A L I K S E E G E K M V L E N N F F V E T M L P S K I M R K L E P E E F A 598

RELLUC.SEQ  A Y L E P F K E K G E V R R P T L S W P R E I P L V K G G K P D V V Q I V R N Y 718
RLUCVER1.SEQ A Y L E P F K E K G E V R R P T L S W P R E I P L V K G G K P D V V Q I V R N Y 718
RLUCVER2.SEQ A Y L E P F K E K G E V R R P T L S W P R E I P L V K G G K P D V V Q I V R N Y 718
RLUCFINL.SEQ A Y L E P F K E K G E V R R P T L S W P R E I P L V K G G K P D V V Q I V R N Y 718

RELLUC.SEQ  N A Y L R A S D D L P K M F I E S D P G F F S N A I V E G A K K F P N T E F V K 838
RLUCVER1.SEQ N A Y L R A S D D L P K M F I E S D P G F F S N A I V E G A K K F P N T E F V K 838
RLUCVER2.SEQ N A Y L R A S D D L P K M F I E S D P G F F S N A I V E G A K K F P N T E F V K 838
RLUCFINL.SEQ N A Y L R A S D D L P K M F I E S D P G F F S N A I V E G A K K F P N T E F V K 838

RELLUC.SEQ  V K G L H F S Q E D A P D E M G K Y I K S F V E R V L K N E Q 931
RLUCVER1.SEQ V K G L H F S Q E D A P D E M G K Y I K S F V E R V L K N E Q 931
RLUCVER2.SEQ V K G L H F S Q E D A P D E M G K Y I K S F V E R V L K N E Q 931
RLUCFINL.SEQ V K G L H F S Q E D A P D E M G K Y I K S F V E R V L K N E Q 931

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Figure 9A

Codon usage in RELLUC

(*Renilla reniformis*; Genbank ACCESSION:M63501; Medline:91239583)

TTT	Phe	11	TCT	Ser	5	TAT	Tyr	12	TGT	Cys	3
TTC	Phe	5	TCC	Ser	1	TAC	Tyr	1	TGC	Cys	0
TTA	Leu	8	TCA	Ser	6	TAA	***	0	TGA	***	0
TTG	Leu	4	TCG	Ser	4	TAG	***	0	TGG	Trp	8
CTT	Leu	8	CCT	Pro	5	CAT	His	9	CGT	Arg	4
CTC	Leu	1	CCC	Pro	0	CAC	His	1	CGC	Arg	0
CTA	Leu	1	CCA	Pro	11	CAA	Gln	6	CGA	Arg	2
CTG	Leu	0	CCG	Pro	2	CAG	Gln	1	CGG	Arg	2
ATT	Ile	12	ACT	Thr	4	AAT	Asn	11	AGT	Ser	2
ATC	Ile	6	ACC	Thr	1	AAC	Asn	2	AGC	Ser	1
ATA	Ile	3	ACA	Thr	1	AAA	Lys	21	AGA	Arg	2
ATG	Met	9	ACG	Thr	0	AAG	Lys	6	AGG	Arg	3
GTT	Val	12	GCT	Ala	5	GAT	Asp	16	GGT	Gly	10
GTC	Val	2	GCC	Ala	3	GAC	Asp	1	GGC	Gly	4
GTA	Val	6	GCA	Ala	8	GAA	Glu	25	GGA	Gly	3
GTG	Val	3	GCG	Ala	3	GAG	Glu	5	GGG	Gly	0

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Figure 9B

Codon Usage in Rluc-final

TTT	Phe	4	TCT	Ser	0	TAT	Tyr	2	TGT	Cys	1
TTC	Phe	12	TCC	Ser	10	TAC	Tyr	11	TGC	Cys	2
TTA	Leu	0	TCA	Ser	1	TAA	***	0	TGA	***	0
TTG	Leu	0	TCG	Ser	0	TAG	***	0	TGG	Trp	8
CTT	Leu	3	CCT	Pro	11	CAT	His	2	CGT	Arg	0
CTC	Leu	6	CCC	Pro	3	CAC	His	8	CGC	Arg	7
CTA	Leu	0	CCA	Pro	4	CAA	Gln	3	CGA	Arg	0
CTG	Leu	13	CCG	Pro	0	CAG	Gln	4	CGG	Arg	3
ATT	Ile	3	ACT	Thr	1	AAT	Asn	2	AGT	Ser	1
ATC	Ile	18	ACC	Thr	4	AAC	Asn	11	AGC	Ser	7
ATA	Ile	0	ACA	Thr	0	AAA	Lys	4	AGA	Arg	2
ATG	Met	9	ACG	Thr	0	AAG	Lys	23	AGG	Arg	1
GTT	Val	2	GCT	Ala	11	GAT	Asp	6	GGT	Gly	3
GTC	Val	8	GCC	Ala	9	GAC	Asp	11	GGC	Gly	7
GTA	Val	0	GCA	Ala	0	GAA	Glu	2	GGA	Gly	3
GTG	Val	13	GCG	Ala	0	GAG	Glu	28	GGG	Gly	4

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Figure 10

Oligonucleotides for the assembly of synthetic *Renilla* luciferase gene

Sense Strand

Oligo name	Oligo sequence from 5' to 3'	
RLS1 (1-40)	AACCATGGCTTCCAAGGTGTACGACCCCGAGCAACGCAAA	(SEQ ID NO:246)
RLS2 (41-80)	CGCATGATCACTGGGCCTCAGTGGTGGGCTCGCTGCAAGC	(SEQ ID NO:247)
RLS3 (81-120)	AAATGAACGTGCTGGACTCCTTCATCAACTACTATGATT	(SEQ ID NO:248)
RLS4 (121-170)	CGAGAAGCACGCCGAGAACGCCGTGATTTTCTGCATGGTAACGCTGCCT	(SEQ ID NO:249)
RLS5 (171-210)	CCAGCTACCTGTGGAGGCACGTCGTGCCTCACATCGAGCC	(SEQ ID NO:250)
RLS6 (211-250)	CGTGGCTAGATGCATCATCCCTGATCTGATCGGAATGGGT	(SEQ ID NO:251)
RLS7 (251-290)	AAGTCCGGCAAGAGCGGGAATGGCTCATATCGCCTCCTGG	(SEQ ID NO:252)
RLS8 (291-330)	ATCACTACAAGTACCTACCGCTTGGTTCGAGCTGCTGAA	(SEQ ID NO:253)
RLS9 (331-370)	CCTTCCAAAGAAAATCATCTTTGTGGGCCACGACTGGGGG	(SEQ ID NO:254)
RLS10 (371-410)	GCTTGTCTGGCCTTTCACACTCCTACGAGCACCAAGACA	(SEQ ID NO:255)
RLS11 (411-450)	AGATCAAGGCCATCGTCCATGCTGAGAGTGTCTGGACGT	(SEQ ID NO:256)
RLS12 (451-495)	GATCGAGTCTGGGACGAGTGGCCTGACATCGAGGAGGATATCG	(SEQ ID NO:257)
RLS13 (496-535)	CCTGATCAAGAGCGAAGAGGGCGAGAAAAATGGTGCTTGAG	(SEQ ID NO:258)
RLS14 (536-575)	AATAACTTCTTCGTCGAGACCATGCTCCCAAGCAAGATCA	(SEQ ID NO:259)
RLS15 (576-620)	TGCGGAAACTGGAGCCTGAGGAGTTCGCTGCCTACCTGGAGCCAT	(SEQ ID NO:260)
RLS16 (621-660)	TCAAGGAGAAGGGCGAGGTTAGACGGCCTACCTCTCCTG	(SEQ ID NO:261)
RLS17 (661-700)	GCCTCGCGAGATCCCTCTCGTTAAGGGAGGCAAGCCCGAC	(SEQ ID NO:262)
RLS18 (701-740)	GTCTGTCAGATTGTGCCGCAACTACAACGCCCTACCTTCGGG	(SEQ ID NO:263)
RLS19 (741-780)	CCAGCGACGATCTGCCTAAGATGTTTCATCGAGTCCGACCC	(SEQ ID NO:264)
RLS20 (781-820)	TGGGTCTTTTCCAACGCTATTGTGCGAGGGAGCTAAGAAG	(SEQ ID NO:265)
RLS21 (821-860)	TTCCCTAACACCGAGTTCGTGAAGGTGAAGGGCCTCCACT	(SEQ ID NO:266)
RLS22 (861-900)	TCAGCCAGGAGGACGCTCCAGATGAAATGGGTAAGTACAT	(SEQ ID NO:267)
RLS23 (901-949)	CAAGAGCTTCGTGGAGCGCGTGTGAAGAACGAGCAGTAATTCTAGAGC	(SEQ ID NO:268)

Anti-sense Strand

Oligo name	Oligo Sequence from 5' to 3'	
RLAS1 (1-29)	GCTCTAGAATTACTGCTCGTTCTTCAGCA	(SEQ ID NO:269)
RLAS2 (30-69)	CGCGCTCCACGAAGCTTGTAGTACTTACCCATTTTCATC	(SEQ ID NO:270)
RLAS3 (70-109)	TGGAGCGTCCCTCCTGGCTGAAGTGGAGGCCCTTCACTTC	(SEQ ID NO:271)
RLAS4 (110-149)	ACGAACTCGGTGTAGGGAACCTTCTTAGCTCCCTCGACAA	(SEQ ID NO:272)
RLAS5 (150-189)	TAGCGTTGGAAAAGAACCAGGGTCGGAATCGATGAACAT	(SEQ ID NO:273)
RLAS6 (190-229)	CTTAGGCAGATCGTCGCTGGCCCGAAGGTAGGCGTTGTAG	(SEQ ID NO:274)
RLAS7 (230-269)	TTGCGGACAATCTGGACGACGTCGGGCTTGCCCTCCCTAA	(SEQ ID NO:275)
RLAS8 (270-309)	CGAGAGGGATCTCGCGAGGCCAGGAGAGGGTAGGCCGTCT	(SEQ ID NO:276)
RLAS9 (310-349)	AACCTCGCCCTTCTCCTTGAATGGCTCCAGGTAGGCAGCG	(SEQ ID NO:277)
RLAS10 (350-394)	AACCTCAGGCTCCAGTTTCCGATGATCTTGCTTGGGAGCATG	(SEQ ID NO:278)
RLAS11 (395-434)	GTCTCGACGAAGAAGTTATTCTCAAGCACCATTTTCTCGC	(SEQ ID NO:279)
RLAS12 (435-474)	CCTCTTCGCTCTTGATCAGGGCGATATCCTCCTCGATGTC	(SEQ ID NO:280)
RLAS13 (475-517)	AGGCCACTCGTCCCAGGACTCGATCACGTCCACGACACTCTCA	(SEQ ID NO:281)
RLAS14 (518-559)	GCATGGACGATGGCCTTGATCTTGCTTGGTGTCTGATAGGAG	(SEQ ID NO:282)
RLAS15 (560-599)	TAGTGAAAGGCCAGACAAGCCCCCAGTCGTGGCCCAAA	(SEQ ID NO:283)
RLAS16 (600-639)	AGATGATTTTCTTTGGAAGGTTTCAAGAGTCAACCAAGC	(SEQ ID NO:284)
RLAS17 (640-679)	GGTGAGGTACTTGTAGTATCCAGGAGGCGATATGAGCCA	(SEQ ID NO:285)
RLAS18 (680-719)	TTCCCGCTCTTGCCGGAATACCATTCGATCAGATCAG	(SEQ ID NO:286)
RLAS19 (720-764)	GGATGATGCATCTAGCCACGGGCTCGATGTGAGGCACGACGTGCC	(SEQ ID NO:287)
RLAS20 (765-804)	TCCACAGGTAGCTGGAGGCAGCGTTACCATGCAGAAAAAT	(SEQ ID NO:288)
RLAS21 (805-849)	CACGGCGTTCTCGGCGTCTTCTCGGAATCATAGTAGTTGATGAA	(SEQ ID NO:289)
RLAS22 (850-889)	GGAGTCCAGCACGTTTCTTGTGCTTGACGCGAGCCACAC	(SEQ ID NO:290)
RLAS23 (890-929)	TGAGGCCAGTGATCATGCGTTTGGCTTGGTGGGTCGT	(SEQ ID NO:291)
RLAS24 (930-949)	ACACCTTGAAGCCATGGTT	(SEQ ID NO:292)

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Figure 11

GRVER51.SEQ A T G A T G A A G C G A A A A G A A C G T G A T C C G G C C C A G A A C 40
LUCPPLYG.SEQ A T G A T G A A G A G A G A G A A A A T G T T A T A T A T G G A C C C G A A C 40
RD1561H9.SEQ A T G A T A A A G C G T G A G A A A A T G T C A T C T A T G G C C C T G A G C 40

GRVER51.SEQ C A C T G C A T C C A C T G G A A G A C C T C A C C G C T G G T G A G A T G C T 80
LUCPPLYG.SEQ C C C T A C A C C C C T T G G A A G A C T T A A C A G C A G G A G A A A T G C T 80
RD1561H9.SEQ C T C T C C A T C C T T T G G A G G A T T T G A C T G C C G G C G A A A T G C T 80

GRVER51.SEQ C T T C C G A G C A C T G C G T A A A C A T A G T C A C C T C C C T C A A G C A 120
LUCPPLYG.SEQ C T T C A G G G C C C T T C G A A A A C A T T C T C A T T T A C C G C A G G C T 120
RD1561H9.SEQ G T T T C G T G C T C T C C G C A A G C A C T C T C A T T T G C C T C A A G C C 120

GRVER51.SEQ C T C G T G G A C G T C G T G G G A G A C G A G A G C C T C T C C T A C A A A G 160
LUCPPLYG.SEQ T T A G T A G A T G T G T T T G G T G A C G A A T C G C T T T C C T A T A A A G 160
RD1561H9.SEQ T T G G T C G A T G T G G T C G G C G A T G A A T C T T T G A G C T A C A A G G 160

GRVER51.SEQ A A T T T T T C G A A G C T A C T G T G C T G T T G G C C C A A A G C C T C C A 200
LUCPPLYG.SEQ A G T T T T T T G A A G C T A C A T G C C T C C T A G C G C A A A G T C T C C A 200
RD1561H9.SEQ A G T T T T T T G A G G C A A C C G T C T T G C T G G C T C A G T C C C T C C A 200

GRVER51.SEQ T A A T T G T G G G T A C A A A A T G A A C G A T G T G G T G A G C A T T T G T 240
LUCPPLYG.SEQ C A A T T G T G G A T A C A A G A T G A A T G A T G T A G T G T C G A T C T G C 240
RD1561H9.SEQ C A A T T G T G G C T A C A A G A T G A A C G A C G T C G T T A G T A T C T G T 240

GRVER51.SEQ G C T G A G A A T A A C A C T C G C T T C T T T A T T C C T G T A A T C G C T G 280
LUCPPLYG.SEQ G C C G A G A A T A A T A A A A G A T T T T T T A T T C C C A T T A T T G C A G 280
RD1561H9.SEQ G C T G A A A A C A A T A C C C G T T T C T T C A T T C C A G T C A T C G C C G 280

GRVER51.SEQ C T T G G T A C A T C G G C A T G A T T G T C G C C C C T G T G A A T G A A T C 320
LUCPPLYG.SEQ C T T G G T A T A T T G G T A T G A T T G T A G C A C C T G T T A A T G A A A G 320
RD1561H9.SEQ C A T G G T A T A T C G G T A T G A T C G T G G C T C C A G T C A A C G A G A G 320

GRVER51.SEQ T T A C A T C C C A G A T G A G C T G T G T A A G G T T A T G G G T A T T A G C 360
LUCPPLYG.SEQ T T A C A T C C C A G A T G A A C T C T G T A A G G T C A T G G G T A T A T C G 360
RD1561H9.SEQ C T A C A T T C C C G A C G A A C T G T G T A A A G T C A T G G G T A T C T C T 360

GRVER51.SEQ A A A C C T C A A A T C G T C T T T A C T A C C A A A A A C A T C T T G A A T A 400
LUCPPLYG.SEQ A A A C C A C A A A T A G T T T T T T G T A C A A A G A A C A T T T T A A A T A 400
RD1561H9.SEQ A A G C C A C A G A T T G T C T T C A C C A C T A A G A A T A T T C T G A A C A 400

GRVER51.SEQ A G G T C T T G G A A G T C C A G T C T C G T A C T A A C T T C A T C A A A C G 440
LUCPPLYG.SEQ A G G T A T T G G A G G T A C A G A G C A G A A C T A A T T T C A T A A A A G 440
RD1561H9.SEQ A A G T C C T G G A A G T C C A A A G C C G C A C C A A C T T T A T T A A G C G 440

GRVER51.SEQ C A T C A T T A T T C T G G A T A C C G T C G A A A A C A T C C A C G G C T G T 480
LUCPPLYG.SEQ G A T C A T C A T A C T T G A T A C T G T A G A A A A C A T A C A C G G T T G T 480
RD1561H9.SEQ T A T C A T C A T C T T G G A C A C T G T G G A G A A T A T T C A C G G T T G C 480

GRVER51.SEQ G A G A G C C T C C C T A A C T T C A T C T C T C G T T A C A G C G A T G G T A 520
LUCPPLYG.SEQ G A A A G T C T T C C C A A T T T T A T T T C T C G T T A T T C G G A T G G A A 520
RD1561H9.SEQ G A A T C T T T G C C T A A T T T C A T C T C T C G C T A T T C A G A C G G C A 520

GRVER51.SEQ A T A T C G C T A A T T T C A A G C C C T T G C A T T T T G A T C C A G T C G A 560
LUCPPLYG.SEQ A T A T T G C C A A C T T C A A A C C T T T A C A T T A C G A T C C T G T T G A 560
RD1561H9.SEQ A C A T C G C A A A C T T T A A A C C A C T C C A C T T C G A C C C T G T G G A 560

Figure 11 (Cont.)

GRVER51.SEQ G C A A G T G G G C T A T T T T G T G C T C C T C C C A C C A C T G G T 600
LUCPPLYG.SEQ G C A A G T G G C A G C T A T C T T A T G T T C G T C A G G C A C T A C T G G A 600
RD1561H9.SEQ A C A A G T T G C A G C C A T T C T G T G T A G C A G C G G T A C T A C T G G A 600

GRVER51.SEQ T T G C C T A A A G G T G T C A T G C A G A C T C A C C A G A A T A T C T G T G 640
LUCPPLYG.SEQ T T A C C G A A A G G T G T A A T G C A A A C T C A C C A A A A T A T T T G T G 640
RD1561H9.SEQ C T C C C A A A G G A G T C A T G C A G A C C A T C A A A A C A T T T G C G 640

GRVER51.SEQ T G C G T T T G A T C C A C G C T C T C G A C C C T C G T G T G G G T A C T C A 680
LUCPPLYG.SEQ T C C G A C T T A T A C A T G C T T T A G A C C C C A G G G C A G G A A C G C A 680
RD1561H9.SEQ T G C G T C T G A T C C A T G C T C T C G A T C C A C G C T A C G G C A C T C A 680

GRVER51.SEQ A T T G A T C C C T G G C G T G A C T G T G C T G G T G T A T C T G C C T T T C 720
LUCPPLYG.SEQ A C T T A T T C C T G G T G T G A C A G T C T T A G T A T A T C T G C C T T T T 720
RD1561H9.SEQ G C T G A T T C C T G G T G T C A C C G T C T T G G T C T A C T T G C C T T T C 720

GRVER51.SEQ T T T C A C G C C T T T G G T T T C T C T A T T A C C C T G G G C T A T T T C A 760
LUCPPLYG.SEQ T T C C A T G C T T T T G G G T T C T C T A T A A A C T T G G G A T A C T T C A 760
RD1561H9.SEQ T T C C A T G C T T T C G G C T T T C A T A T T A C T T T G G G T T A C T T T A 760

GRVER51.SEQ T G G T C G G C T T G C G T G T C A T C A T G T T T C G T C G C T T C G A C C A 800
LUCPPLYG.SEQ T G G T G G G T C T T C G T G T T A T C A T G T T A A G A C G A T T T G A T C A 800
RD1561H9.SEQ T G G T C G G T C T C C G C G T G A T T A T G T T C C G C C G T T T T G A T C A 800

GRVER51.SEQ A G A A G C C T T C T T G A A G G C T A T T C A A G A C T A C G A G G T G C G T 840
LUCPPLYG.SEQ A G A A G C A T T T C T A A A A G C T A T T C A G G A T T A T G A A G T T C G A 840
RD1561H9.SEQ G G A G C T T T C T T G A A A G C C A T C C A A G A T T A T G A A G T C C G C 840

GRVER51.SEQ T C C G T G A T C A A C G T C C C T T C A G T C A T T T T G T T C C T G A G C A 880
LUCPPLYG.SEQ A G T G T A A T T A A C G T T C C A G C A A T A A T A T T G T T C T T A T C G A 880
RD1561H9.SEQ A G T G T C A T C A A C G T G C C T A G C G T G A T C C T G T T T T T G T C T A 880

GRVER51.SEQ A A T C T C C T T T G G T T G A C A A G T A T G A T C T G A G C A G C T T G C G 920
LUCPPLYG.SEQ A A A G T C C T T T G G T T G A C A A A T A C G A T T T A T C A A G T T T A A G 920
RD1561H9.SEQ A G A G C C C A C T C G T G G A C A A G T A C G A C T T G T C T T C A C T G C G 920

GRVER51.SEQ T G A G C T G T G C T G T G G C G C T G C T C C T T T G G C C A A A G A A G T G 960
LUCPPLYG.SEQ G G A A T T G T G T T G C G G T G C G G C A C C A T T A G C A A A A G A A G T T 960
RD1561H9.SEQ T G A A T T G T G T T G C G G T G C G C T C C A C T G G C T A A G G A G G T C 960

GRVER51.SEQ G C C G A G G T C G C T G C T A A G C G T C T G A A C C T C C C T G G T A T C C 1000
LUCPPLYG.SEQ G C T G A G G T T G C A G T A A A A C G A T T A A A C T T G C C A G G A A T T C 1000
RD1561H9.SEQ G C T G A A G T G G C C G C A A A C G C T T G A A T C T T C C A G G G A T T C 1000

GRVER51.SEQ G C T G C G G T T T T G G T T T G A C T G A G A G C A C T T C T G C T A A C A T 1040
LUCPPLYG.SEQ G C T G T G G A T T T G G T T T G A C A G A A T C T A C T T C A G C T A A T A T 1040
RD1561H9.SEQ G T T G T G G C T T C G G C C T C A C C G A A T C T A C C A G T G C G A T T A T 1040

GRVER51.SEQ C C A T A G C T T G C G A G A C G A G T T T A A G T C T G G T A G C C T G G G T 1080
LUCPPLYG.SEQ A C A C A G T C T T G G G G A T G A A T T T A A A T C A G G A T C A C T T G G A 1080
RD1561H9.SEQ C C A G A C T C T C G G G G A T G A G T T T A A G A G C G G C T C T T T G G G C 1080

GRVER51.SEQ C G C G T G A C T C C T C T T A T G G C T G C A A A G A T C G C C G A C C G T G 1120
LUCPPLYG.SEQ A G A G T T A C T C C T T T A A T G G C A G C T A A A A T A G C A G A T A G G G 1120
RD1561H9.SEQ C G T G T C A C T C C A C T C A T G G C T G C T A A G A T C G C T G A T C G C G 1120

Figure 11 (Cont.)

GRVER51.SEQ A G A C G G C A G C A C T G G G C C C A A A T C A T C G G T G A A T T 1160
LUCPPLYG.SEQ A A A C T G G T A A A G C A T T G G G A C C A A A T C A A G T T G G T G A A T T 1160
RD1561H9.SEQ A A A C T G G T A A G G C T T T G G G C C C G A A C C A A G T G G G C G A G C T 1160

GRVER51.SEQ G T G T A T T A A G G G C C C T A T G G T C T C T A A A G G C T A C G T G A A C 1200
LUCPPLYG.SEQ A T G C G T T A A A G G T C C C A T G G T A T C G A A A G G T T A C G T G A A C 1200
RD1561H9.SEQ G T G T A T C A A A G G C C C T A T G G T G A G C A A G G G T T A T G T C A A T 1200

GRVER51.SEQ A A T G T G G A G G C C A C T A A A G A A G C C A T T G A T G A T G A T G G C T 1240
LUCPPLYG.SEQ A A T G T A G A A G C T A C C A A A G A A G C T A T T G A T G A T G A T G G T T 1240
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GRVER51.SEQ T T T T G C T G A A G A A C C C T T G T A T C C G C G A C G T G G C C G T C G T 1400
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GRVER51.SEQ A G C A A C T C C T C G A A A A A G C T G G C G G C 1626
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Figure 12

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RD1561H9.SEQ M I K R E K N V I Y G P E P L H P L E D L T A G E M L F R A L R K H S H L P Q A 118

GRVER51.SEQ L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238
LUCPPPLYG.SEQ L V D V F G D E S L S Y K E F F E A T C L L A Q S L H N C G Y K M N D V V S I C 238
RD1561H9.SEQ L V D V V G D E S L S Y K E F F E A T V L L A Q S L H N C G Y K M N D V V S I C 238

GRVER51.SEQ A E N N T R F F I P V I A A W Y I G M I V A P V N E S Y I P D E L C K V M G I S 358
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GRVER51.SEQ K P Q I V F T T K N I L N K V L E V Q S R T N F I K R I I I L D T V E N I H G C 478
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GRVER51.SEQ Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
LUCPPPLYG.SEQ Y K G S Q V A P A E L E E I L L K N P C I R D V A V V G I P D L E A G E L P S A 1438
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GRVER51.SEQ R N V T G K I T R K E L L K Q L L E K A G G 1624
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Renilla luciferase gene in pGL3 series

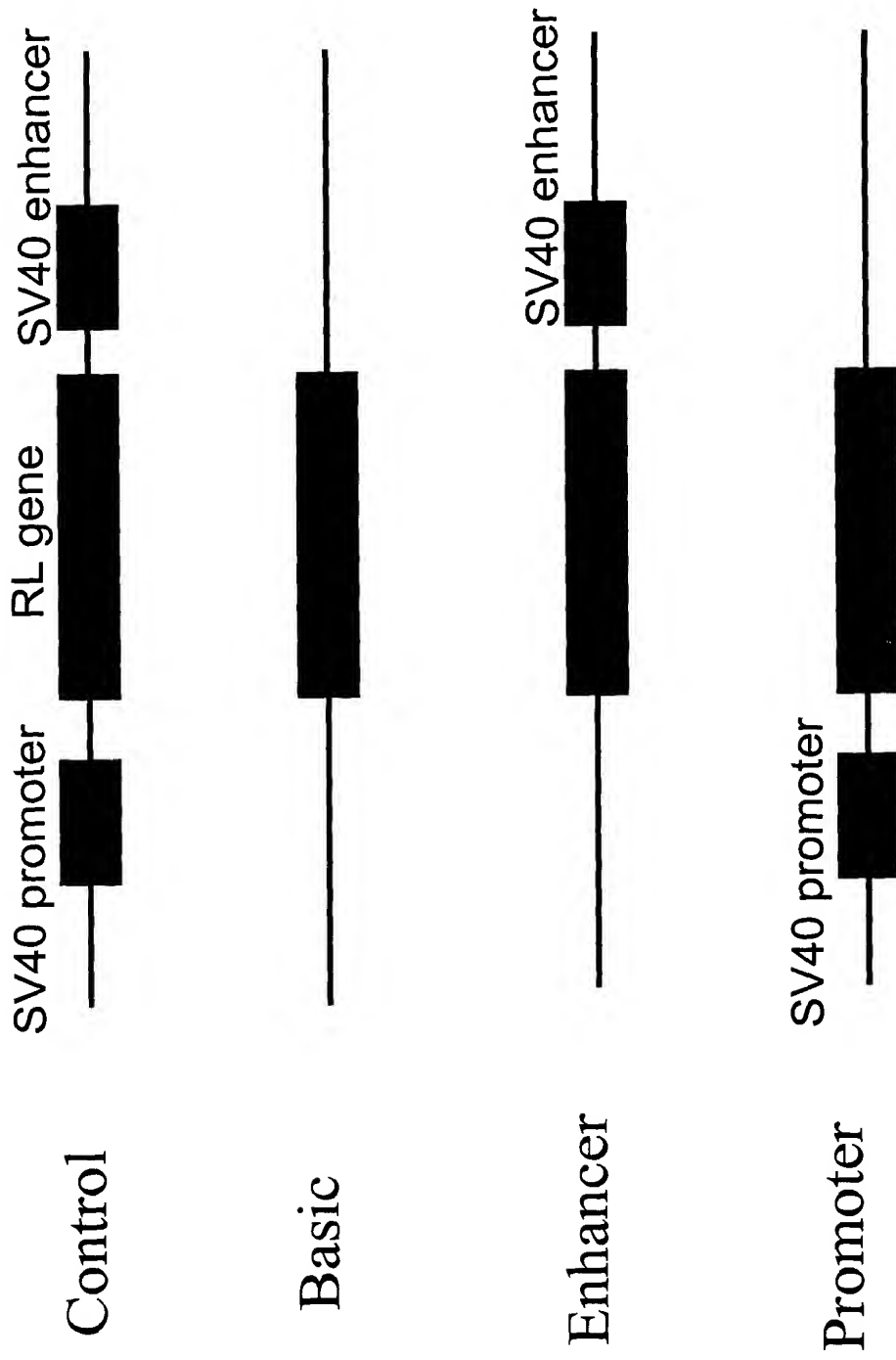
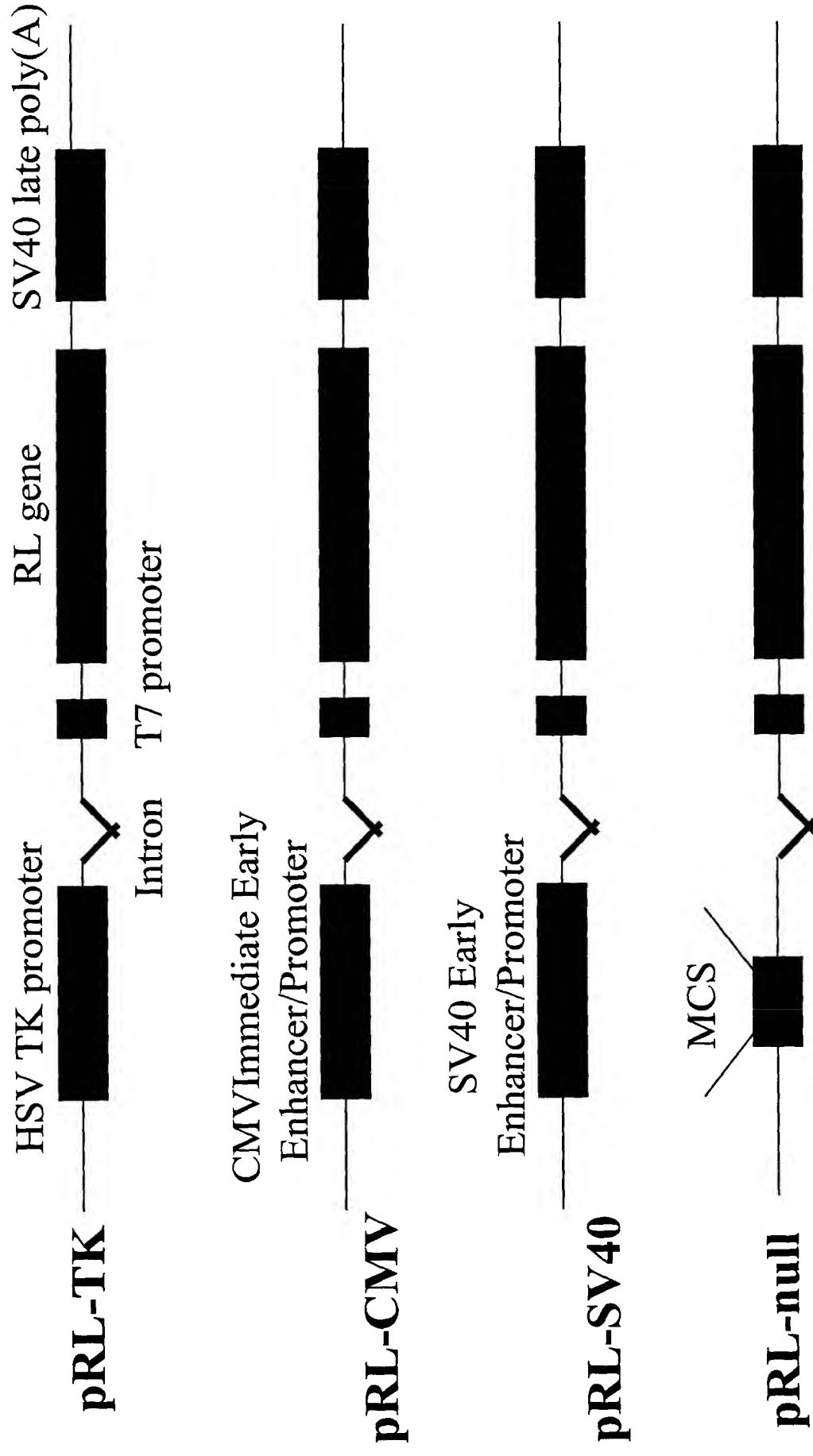


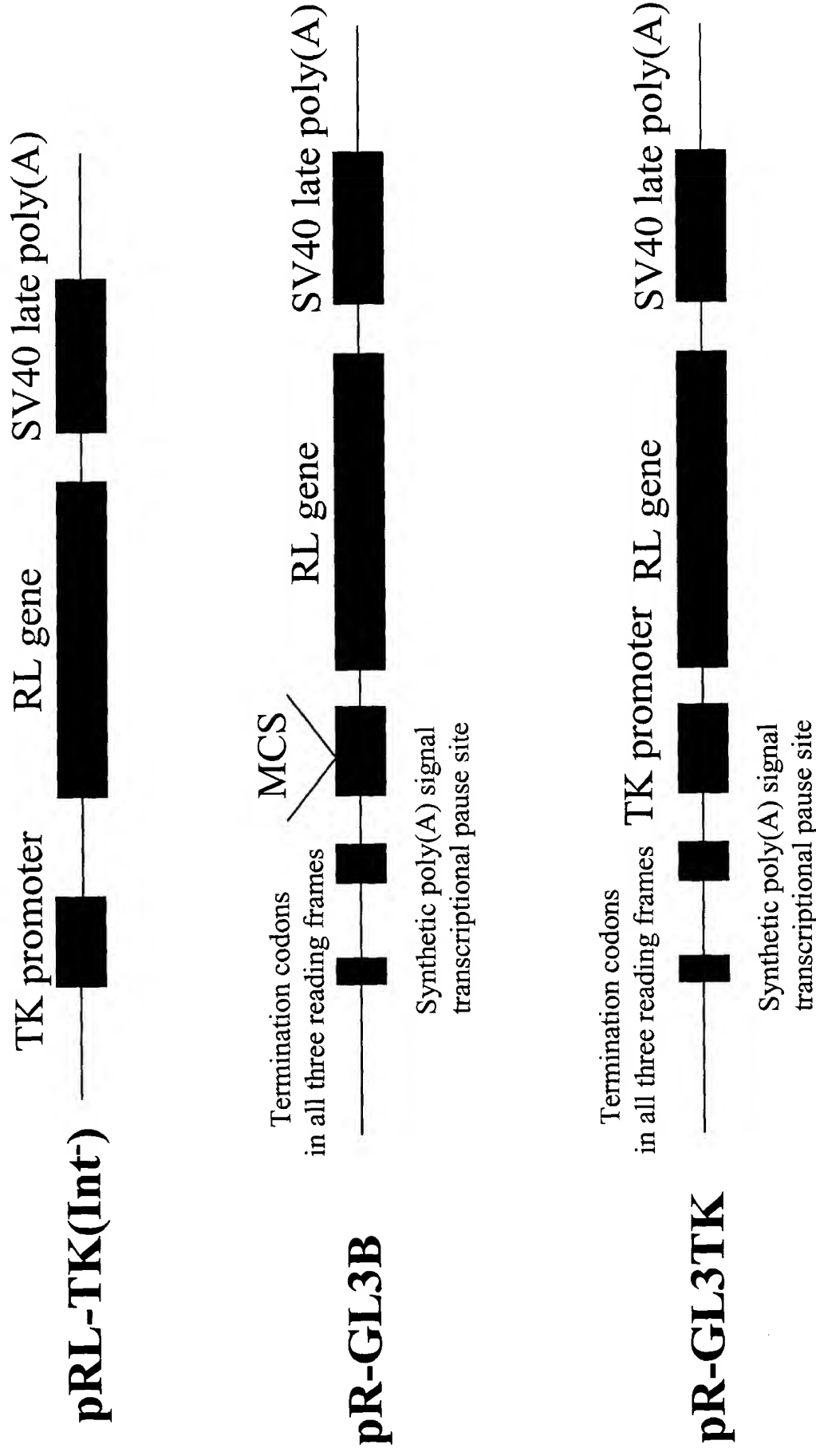
Fig 13A

Figure 13^β- RL Co-Reporter Vector Series



^B

Figure 13 (Continued)



Half-life of RL-synthetic and RL-native in CHO Cells

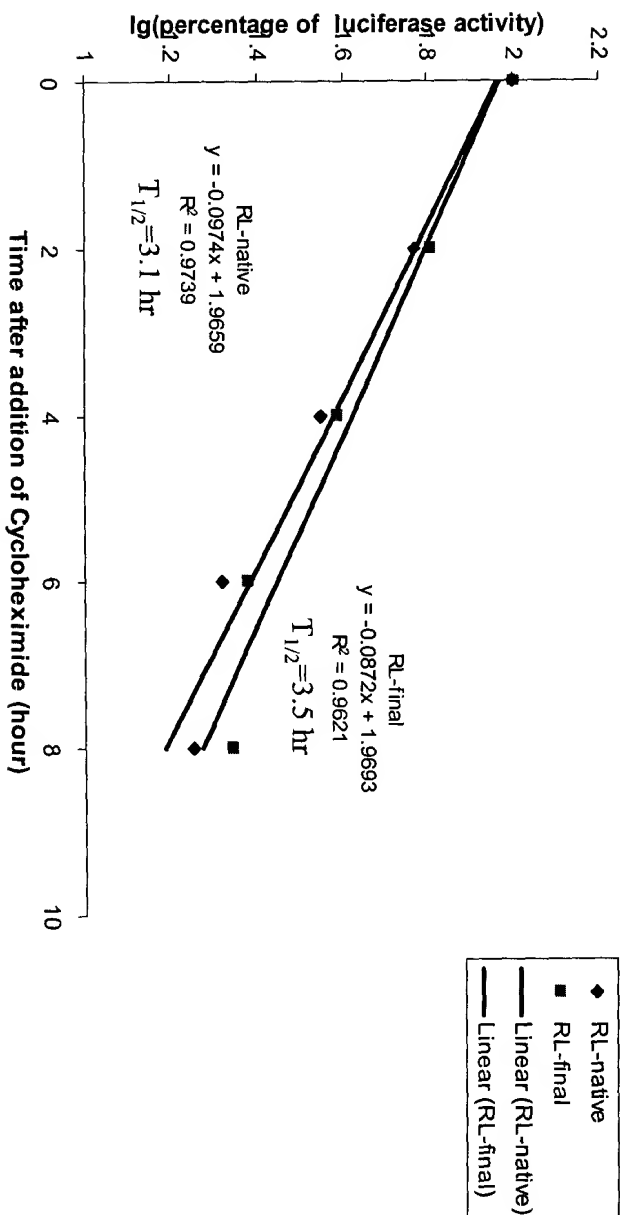


Fig 4

TNT (RL-final versus RL-native)

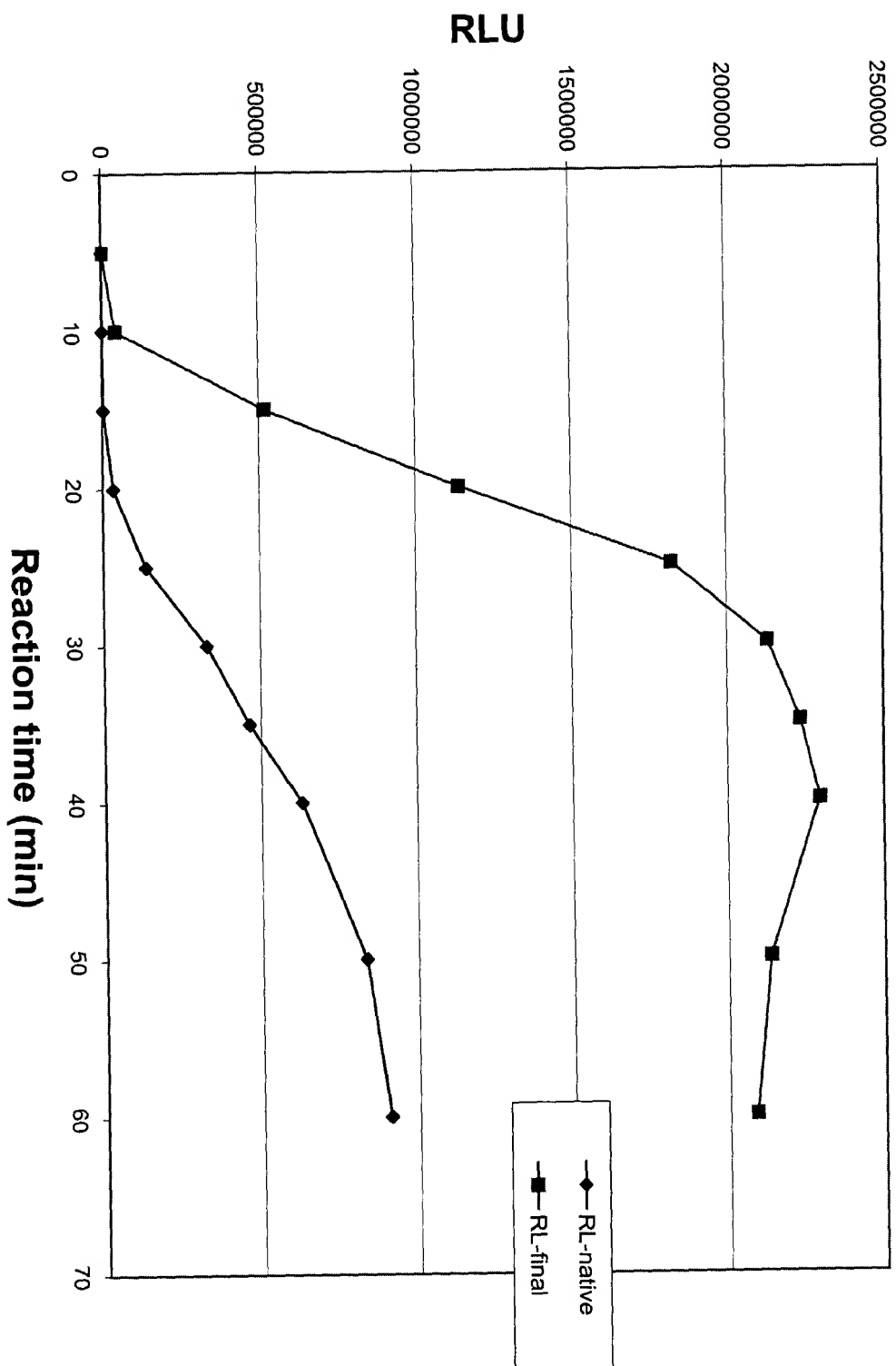
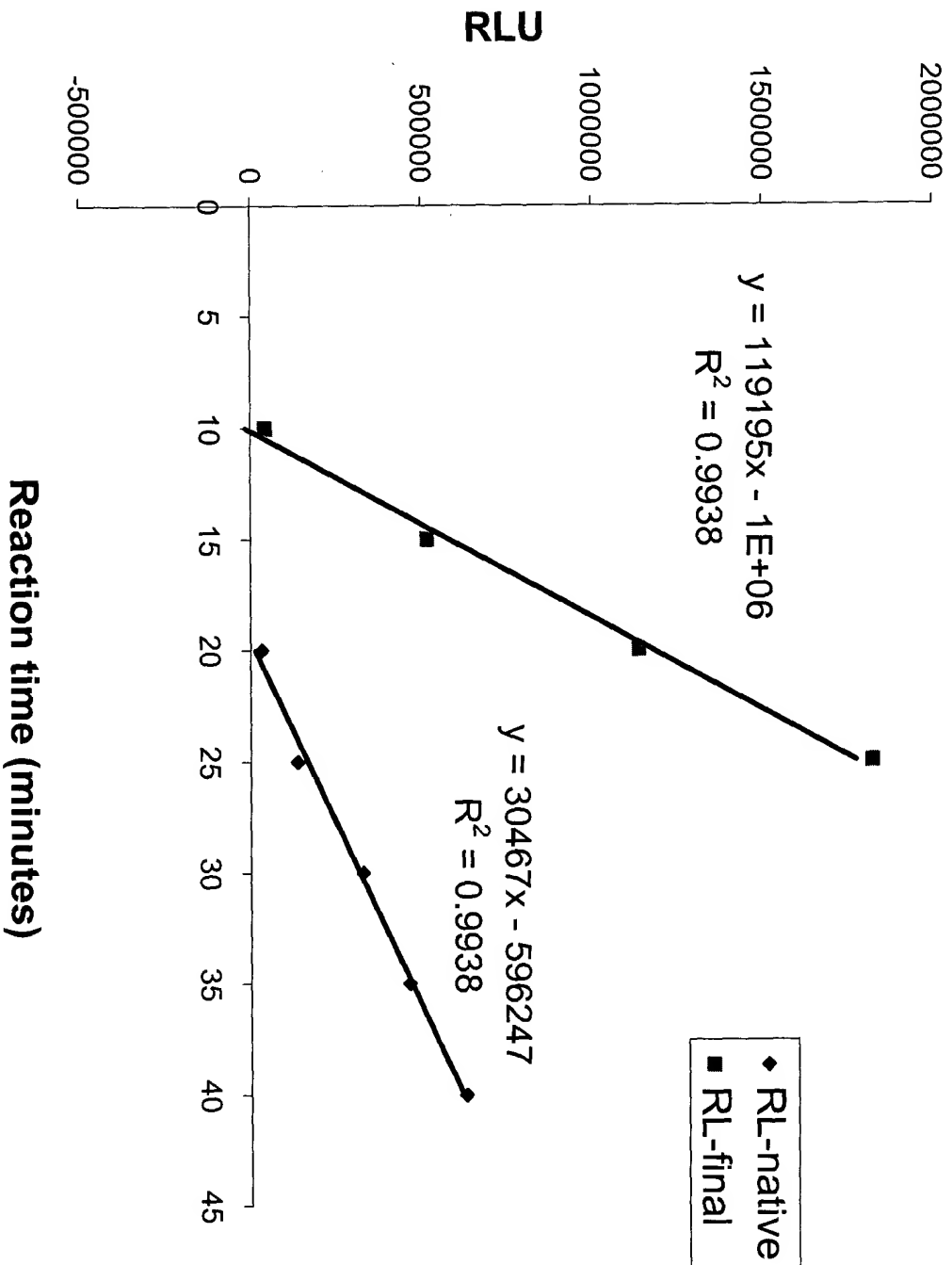


Fig15A

09645706 . 082400

TNT (RL-final versus RL-native, linear range)



09645706.082400

Fig15B

In vitro translation of RNAs of native RL and RL-final (30°C)

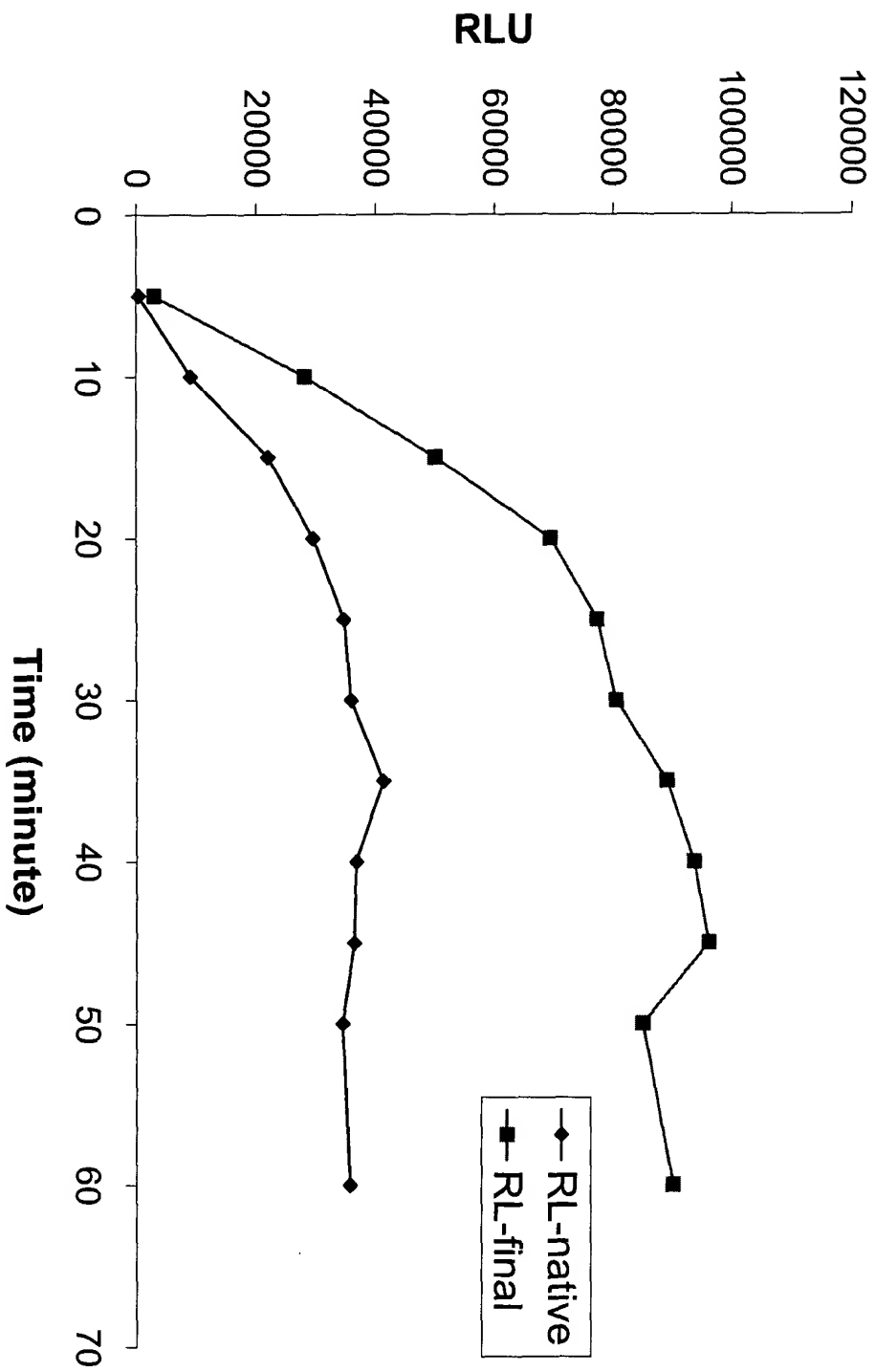


Fig15C

09645706.082400

In vitro translation of RNAs of native RL and RL-final (30 °C, linear range)

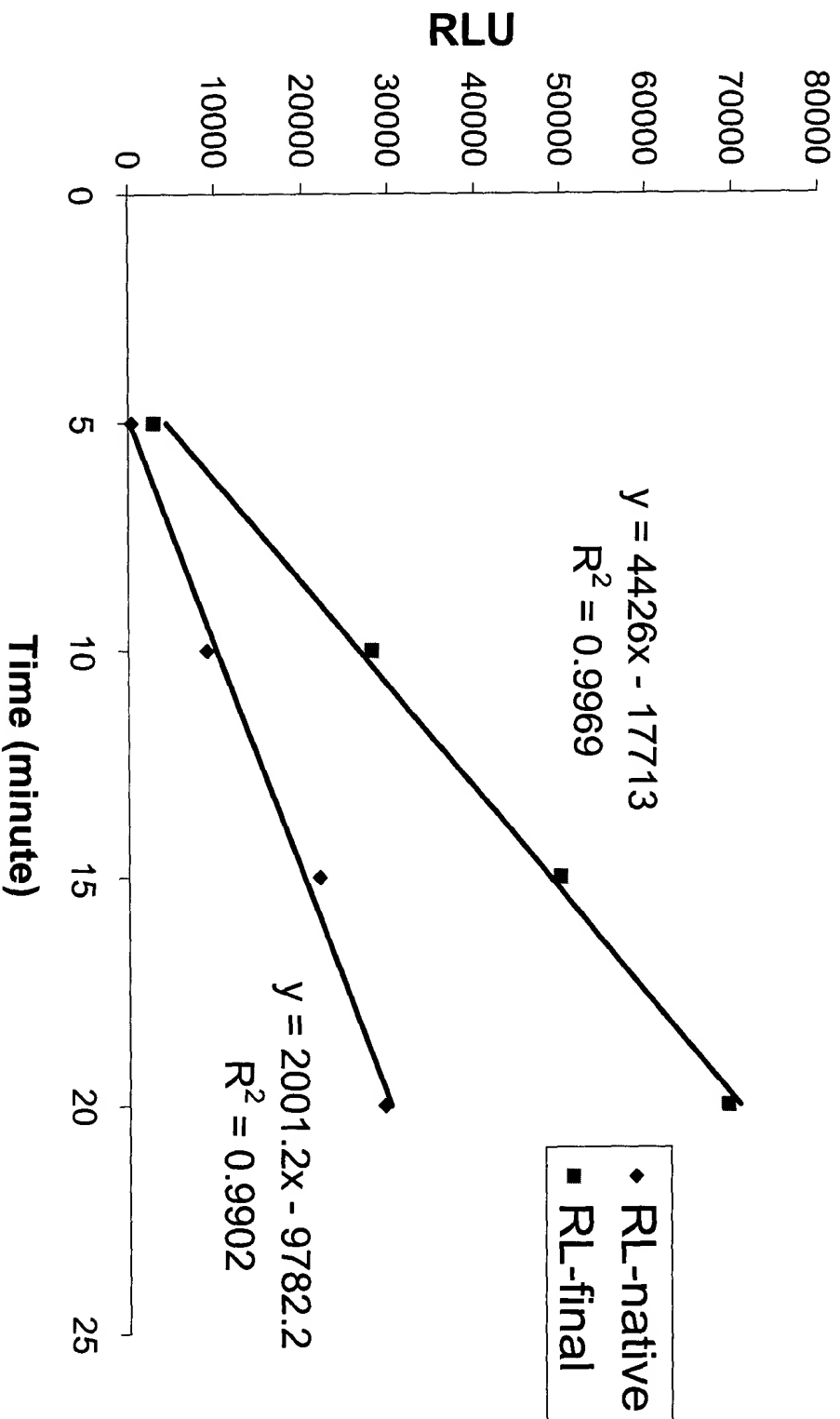


Fig 15D

In vitro translation using wheat germ extract

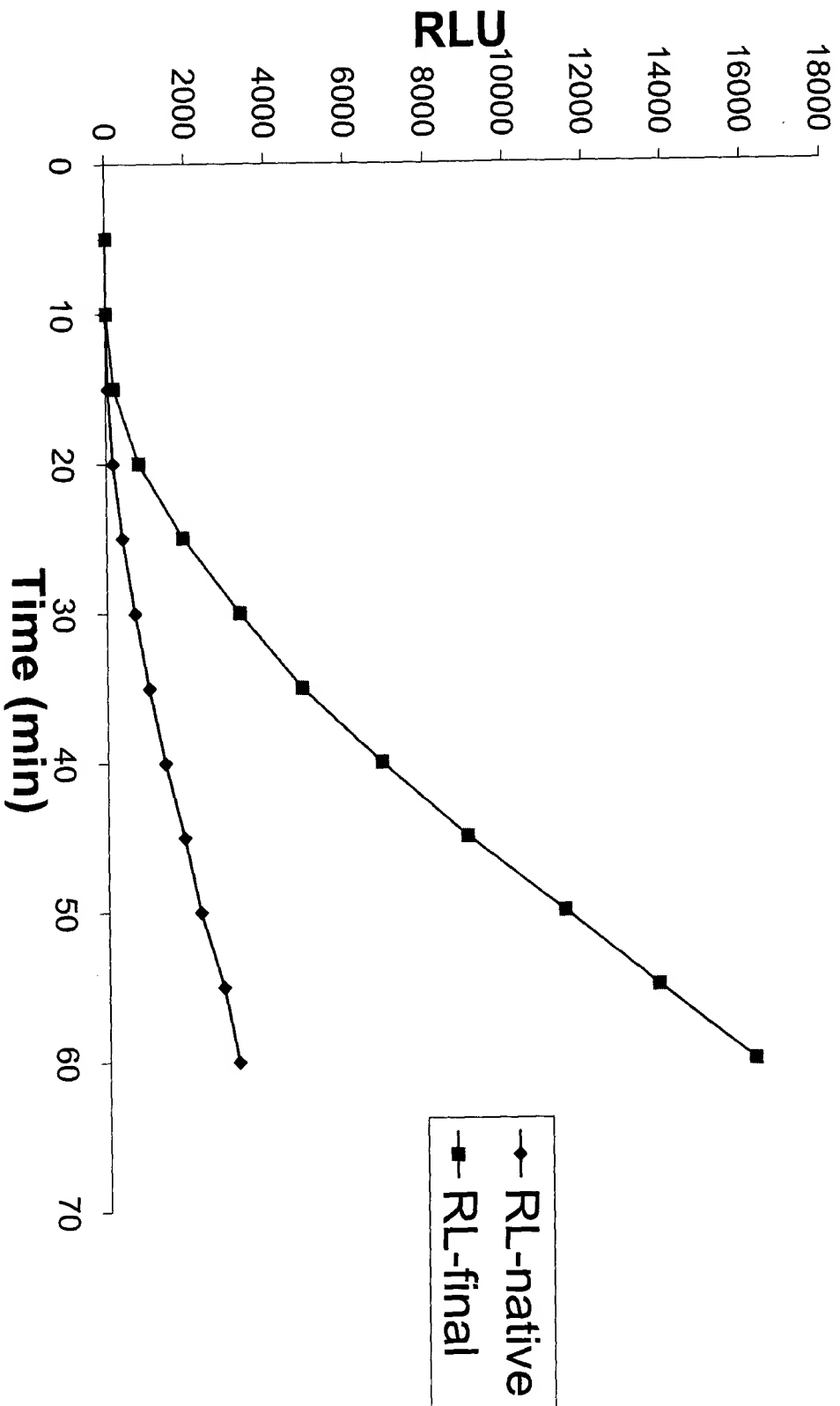


Fig15E

In vitro translation using wheat germ extract (linear range)

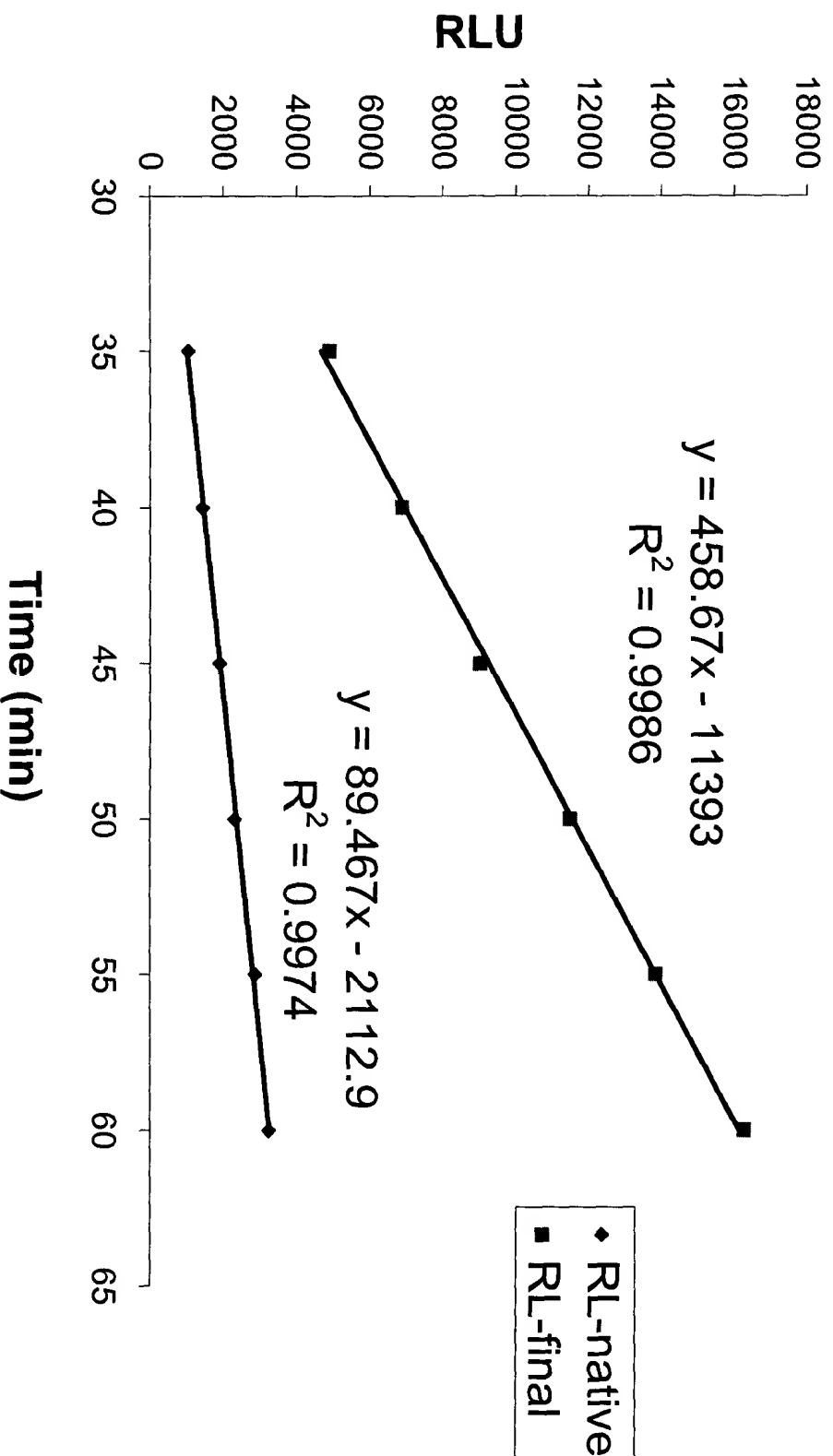


Fig 15F

09645706_032400

Renilla expression

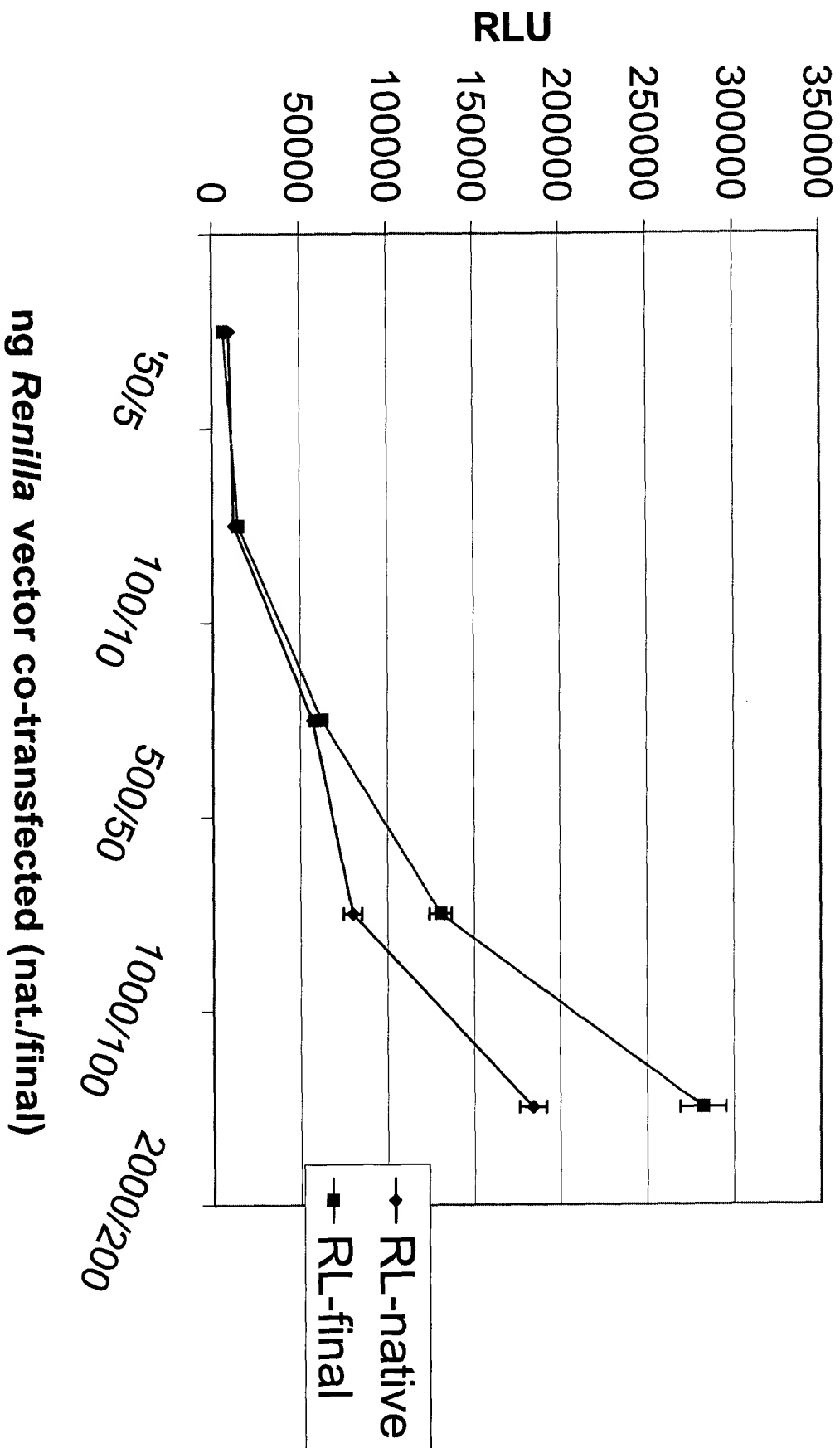


Fig 16f

Effect of firefly expression with increasing amounts of TK vector co-transfected

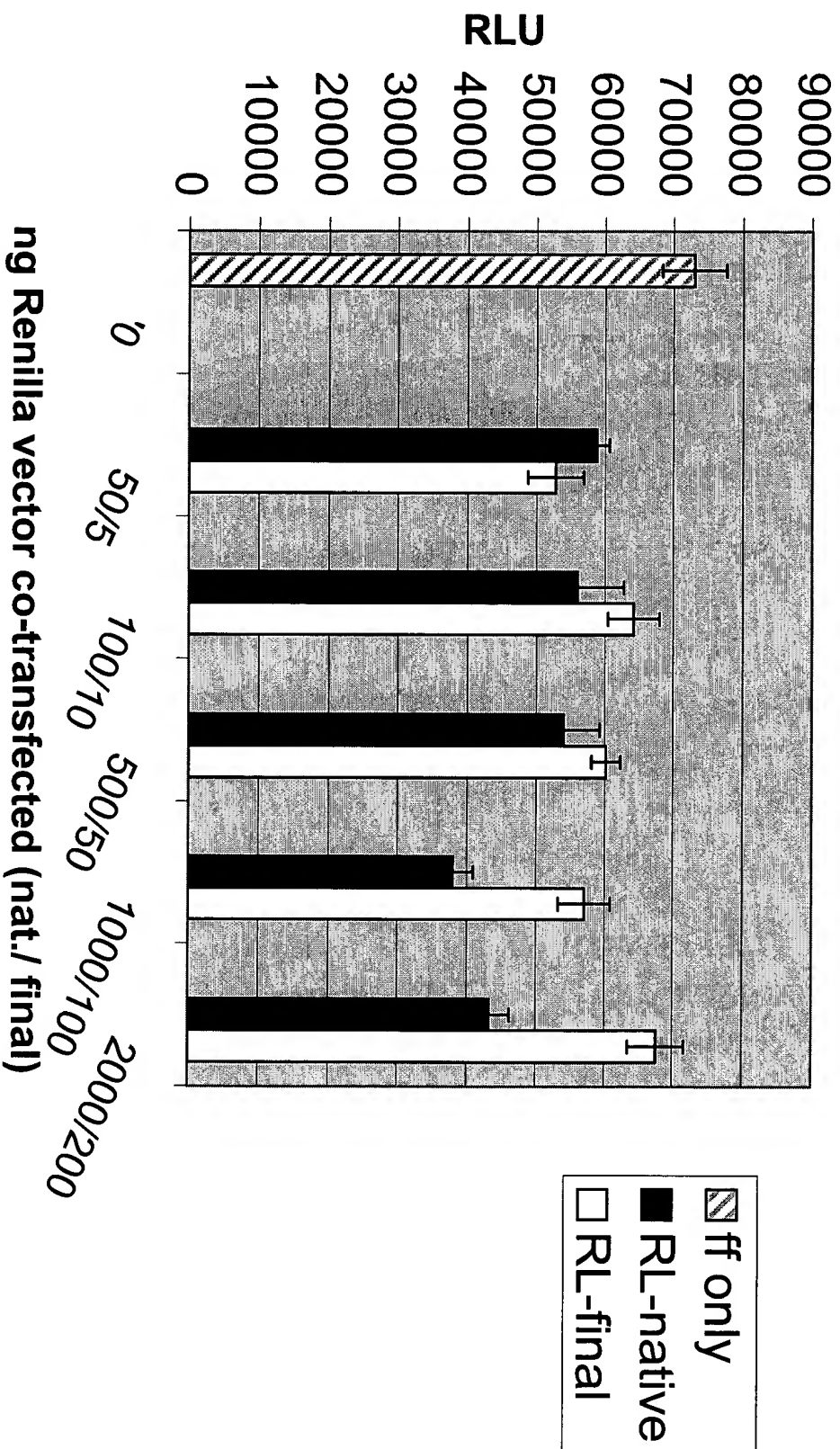
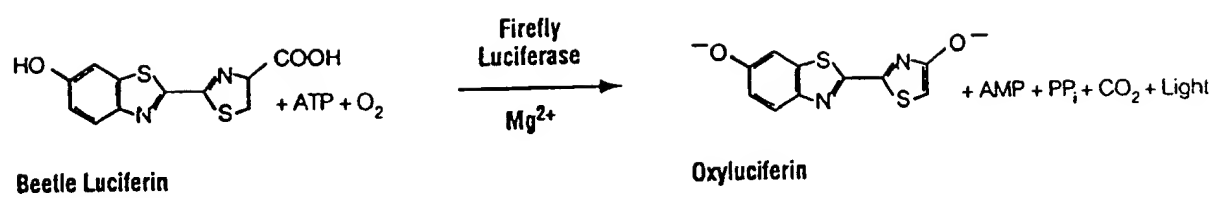


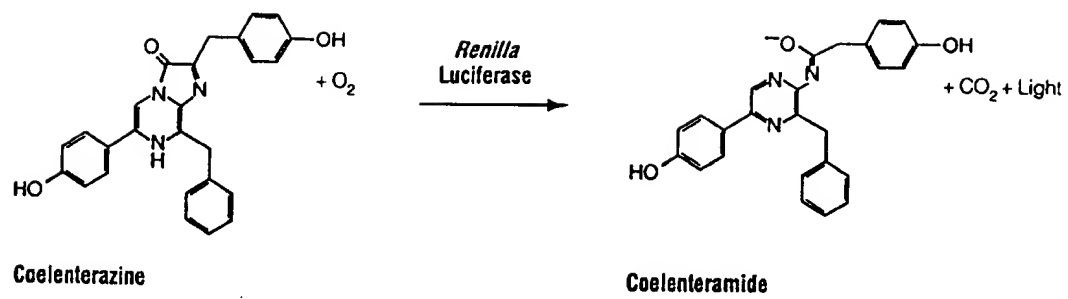
Fig 16B

Figure 17 A



004280-90754960

Figure 7173



09645706.082400

09645706-082400

GRver5.1 DNA sequence of pGL3 vectors

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GTCGCCCCCTGTGAATGAATCTTACATCCCAGATGAGCTGTGTAAGGTTAT 350
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TGCTGGTGTATCTGCCCTTTCTTTACGCCCTTTGGTTTCTCTATTACCTG 750
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SEQ ID NO: 297

Figure 18A

004230-034950

RDver5.1 DNA sequence of pGL3 vectors

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SEQ ID NO: 299

09645706.082400

RD1561H9 DNA sequenc of pGL3 vectors

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CTCCATCCCTCGTAACGTAACAGGCAAAATTACCCGCAAGGAGCTGTTGA 1600
ACAATTGTTGGTGAAGGCCGGCGGT 1626
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SEQ ID NO: 301

GRver5.1 protein sequence of pGL3 vectors

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LDTVENIHGCESLPNFISRYSDGNIANFKPLHFDPEQVAAILCSSGTTG 200
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GYFMVGLRVIMFRRFDQEAFLKAIQDYEVRSVINVPSVILFLSKSPLVDK 300
YDLSSLRELCCGAAPLAKEVAEVAAKRLNLPGIRCGFGLTESTSANIHSL 350
RDEFKSGSLGRVTPLMAAKIADRETGKALGPNQVGELCIKGPMSKGYVN 400
NVEATKEAIDDDGWLHSGDFGYDEDEHFYVVDYKELIKYKGSQVAPAE 450
LEEILLKNPCIRDVAVVGIPDLEAGELPSAFVVKQPGKEITAKEVYDYL 500
ERVSHTKYLRGGVRFVDSIPRNVTKITRKELLKQLLEKAGG 542

SEQ ID NO: 298

RDver5.1 protein sequence of pGL3 vectors

MVKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQALVDVVGDESL 50
SYKEFFEATVLLAQSLHNCGYKMNDVVSICAENNTRFFIPVIAAWYIGMI 100
VAPVNESYIPDELCKVMGISKQPQIVFTTKNILNKVLEVQSRNFIKRIII 150
LDTVENIHGCESLPNFISRYSDGNIANFKPLHFDPEQVAAILCSSGTTG 200
LPKGVMTQTHQNICVRLIHALDPRVGTQLIPGVTVLVYLPFFHAFGFHITL 250
GYFMVGLRVIMFRRFDQEAFLKAIQDYEVRSVINVPSVILFLSKSPLVDK 300
YDLSSLRELCCGAAPLAKEVAEVAAKRLNLPGIRCGFGLTESTSAIIQSL 350
RDEFKSGSLGRVTPLMAAKIADRETGKALGPNQVGELCIKGPMSKGYVN 400
NVEATKEAIDDDGWLHSGDFGYDEDEHFYVVDYKELIKYKGSQVAPAE 450
LEEILLKNPCIRDVAVVGIPDLEAGELPSAFVVKQPGKEITAKEVYDYL 500
ERVSHTKYLRGGVRFVDSIPRNVTKITRKELLKQLLEKAGG 542

SEQ ID NO: 300

RD1561H9 protein sequence of pGL3 vectors

MVKREKNVIYGPEPLHPLEDLTAGEMLFRALRKHSHLPQALVDVVGDESL 50
SYKEFFEATVLLAQSLHNCGYKMNDVVSICAENNTRFFIPVIAAWYIGMI 100
VAPVNESYIPDELCKVMGISKQPQIVFTTKNILNKVLEVQSRNFIKRIII 150
LDTVENIHGCESLPNFISRYSDGNIANFKPLHFDPEQVAAILCSSGTTG 200
LPKGVMTQTHQNICVRLIHALDPRVGTQLIPGVTVLVYLPFFHAFGFHITL 250
GYFMVGLRVIMFRRFDQEAFLKAIQDYEVRSVINVPSVILFLSKSPLVDK 300
YDLSSLRELCCGAAPLAKEVAEVAAKRLNLPGIRCGFGLTESTSAIIQTL 350
GDEFKSGSLGRVTPLMAAKIADRETGKALGPNQVGELCIKGPMSKGYVN 400
NVEATKEAIDDDGWLHSGDFGYDEDEHFYVVDYKELIKYKGSQVAPAE 450
LEEILLKNPCIRDVAVVGIPDLEAGELPSAFVVKQPGTEITAKEVYDYL 500
ERVSHTKYLRGGVRFVDSIPRNVTKITRKELLKQLLVKAGG 542

SEQ ID NO: 308

004280-302960